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(54) Title: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

(57) Abstract: Novel polynucleotides and the proteins encoded thereby are disclosed.

5                    **SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM****BACKGROUND OF THE INVENTION**

Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs and interleukins) has matured rapidly over the past decade. The  
10 now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as  
15 signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity by virtue of their secreted nature in the case of leader sequence cloning, or by virtue of the cell or tissue source in the case of PCR-based techniques. It is to these proteins and the polynucleotides  
20 encoding them that the present invention is directed.

**SUMMARY OF THE INVENTION**

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25                    (a)      a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1;
- (b)      a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 282 to nucleotide 565;
- (c)      a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 342 to nucleotide 565;
- 30                    (d)      a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AX65\_22 deposited with the ATCC under accession number 98196;
- (e)      a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AX65\_22 deposited with the ATCC under accession number 98196;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AX65\_22 deposited with the ATCC under accession number 98196;

5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AX65\_22 deposited with the ATCC under accession number 98196;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:2;

10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:2;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

15 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:1.

20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:1 from nucleotide 282 to nucleotide 565; the nucleotide sequence of SEQ ID NO:1 from nucleotide 342 to nucleotide 565; the nucleotide sequence of the full-length protein coding sequence of clone AX65\_22 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone AX65\_22 deposited with the ATCC under accession  
25 number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AX65\_22 deposited with the ATCC under accession number 98196. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably  
30 twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID NO:2.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID  
35 NO:1 and SEQ ID NO:3.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:1;

(ab) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and

(ac) the nucleotide sequence of the cDNA insert of clone AX65\_22 deposited with the ATCC under accession number 98196;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:1;

(bb) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and

(bc) the nucleotide sequence of the cDNA insert of clone AX65\_22 deposited with the ATCC under accession number 98196;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:1 and SEQ ID NO:3, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:1 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ



ID NO:1 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:1. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1 from nucleotide 282 to nucleotide 565, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence  
5 of SEQ ID NO:1 from nucleotide 282 to nucleotide 565, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 282 to nucleotide 565. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1 from nucleotide 342 to nucleotide 565, and extending contiguously from a nucleotide sequence corresponding to the 5'  
10 end of said sequence of SEQ ID NO:1 from nucleotide 342 to nucleotide 565, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 342 to nucleotide 565.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:  
15 (a) the amino acid sequence of SEQ ID NO:2;  
(b) a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2; and  
(c) the amino acid sequence encoded by the cDNA insert of clone AX65\_22 deposited with the ATCC under accession number 98196;  
20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:2. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a protein comprising  
25 a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID NO:2.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:  
(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:4;  
30 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:4 from nucleotide 192 to nucleotide 2318;  
(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:4 from nucleotide 653 to nucleotide 825;

- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BD335\_14 deposited with the ATCC under accession number 98196;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BD335\_14 deposited with the ATCC under accession number 98196;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BD335\_14 deposited with the ATCC under accession number 98196;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BD335\_14 deposited with the ATCC under accession number 98196;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:5;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:5 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:5;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:4.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:4 from nucleotide 192 to nucleotide 2318; the nucleotide sequence of SEQ ID NO:4 from nucleotide 653 to nucleotide 825; the nucleotide sequence of the full-length protein coding sequence of clone BD335\_14 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone BD335\_14 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BD335\_14 deposited with the ATCC under accession number 98196. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:5 from amino acid 148 to amino acid 240. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid

sequence of SEQ ID NO:5 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:5, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:5 having biological activity, the fragment comprising the amino acid sequence from amino  
5 acid 349 to amino acid 358 of SEQ ID NO:5.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:4.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 10 (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 15 (aa) SEQ ID NO:4, but excluding the poly(A) tail at the 3' end of SEQ ID NO:4; and
    - (ab) the nucleotide sequence of the cDNA insert of clone BD335\_14 deposited with the ATCC under accession number 98196;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - 20 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group  
25 consisting of:
    - (ba) SEQ ID NO:4, but excluding the poly(A) tail at the 3' end of SEQ ID NO:4; and
    - (bb) the nucleotide sequence of the cDNA insert of clone BD335\_14 deposited with the ATCC under accession number 98196;
    - 30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
    - (iii) amplifying human DNA sequences; and
    - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide  
35 sequence corresponding to the cDNA sequence of SEQ ID NO:4, and extending contiguously from

a nucleotide sequence corresponding to the 5' end of SEQ ID NO:4 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:4, but excluding the poly(A) tail at the 3' end of SEQ ID NO:4. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:4 from nucleotide 192  
5 to nucleotide 2318, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:4 from nucleotide 192 to nucleotide 2318, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:4 from nucleotide 192 to nucleotide 2318. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:4 from  
10 nucleotide 653 to nucleotide 825, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:4 from nucleotide 653 to nucleotide 825, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:4 from nucleotide 653 to nucleotide 825.

In other embodiments, the present invention provides a composition comprising a protein,  
15 wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:5;
- (b) the amino acid sequence of SEQ ID NO:5 from amino acid 148 to amino acid 240;
- (c) a fragment of the amino acid sequence of SEQ ID NO:5, the fragment  
20 comprising eight contiguous amino acids of SEQ ID NO:5; and
- (d) the amino acid sequence encoded by the cDNA insert of clone BD335\_14 deposited with the ATCC under accession number 98196;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:5 or the amino acid sequence of SEQ ID NO:5  
25 from amino acid 148 to amino acid 240. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:5 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:5, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:5 having biological activity, the fragment comprising  
30 the amino acid sequence from amino acid 349 to amino acid 358 of SEQ ID NO:5.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7  
35 from nucleotide 206 to nucleotide 391;

- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BG241\_1 deposited with the ATCC under accession number 98196;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BG241\_1 deposited with the ATCC under accession number 98196;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BG241\_1 deposited with the ATCC under accession number 98196;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BG241\_1 deposited with the ATCC under accession number 98196;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:8;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:8;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:7.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:7 from nucleotide 206 to nucleotide 391; the nucleotide sequence of the full-length protein coding sequence of clone BG241\_1 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone BG241\_1 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BG241\_1 deposited with the ATCC under accession number 98196. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:8, or a polynucleotide encoding a protein comprising a fragment of the amino acid

sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID NO:8.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:7, SEQ ID NO:6, and SEQ ID NO:9.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X  
SSC at 65 degrees C to a nucleotide sequence selected from the group consisting  
10 of:

(aa) SEQ ID NO:6;

(ab) SEQ ID NO:7;

(ac) SEQ ID NO:9, but excluding the poly(A) tail at the 3'  
end of SEQ ID NO:9; and

(ad) the nucleotide sequence of the cDNA insert of clone  
15 BG241\_1 deposited with the ATCC under accession number 98196;

(ii) hybridizing said probe(s) to human genomic DNA in conditions  
at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

20 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in  
6X SSC at 65 degrees C to a nucleotide sequence selected from the group  
consisting of:

(ba) SEQ ID NO:6;

(bb) SEQ ID NO:7;

(bc) SEQ ID NO:9, but excluding the poly(A) tail at the 3'  
end of SEQ ID NO:9; and

(bd) the nucleotide sequence of the cDNA insert of clone  
30 BG241\_1 deposited with the ATCC under accession number 98196;

(ii) hybridizing said primer(s) to human genomic DNA in conditions  
at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:6, SEQ ID NO:7, and SEQ ID NO:9, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:6 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:7 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:7. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7 from nucleotide 206 to nucleotide 391, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:7 from nucleotide 206 to nucleotide 391, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 206 to nucleotide 391.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:8;
- (b) a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8; and
- (c) the amino acid sequence encoded by the cDNA insert of clone BG241\_1 deposited with the ATCC under accession number 98196;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:8. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:8, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID NO:8.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:10;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:10 from nucleotide 302 to nucleotide 1762;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:10 from nucleotide 389 to nucleotide 1762;

- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:10 from nucleotide 1723 to nucleotide 2050;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BL187\_4 deposited with the ATCC under accession number 98196;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BL187\_4 deposited with the ATCC under accession number 98196;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BL187\_4 deposited with the ATCC under accession number 98196;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BL187\_4 deposited with the ATCC under accession number 98196;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:11;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:11 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:11;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:10.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:10 from nucleotide 302 to nucleotide 1762; the nucleotide sequence of SEQ ID NO:10 from nucleotide 389 to nucleotide 1762; the nucleotide sequence of SEQ ID NO:10 from nucleotide 1723 to nucleotide 2050; the nucleotide sequence of the full-length protein coding sequence of clone BL187\_4 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone BL187\_4 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BL187\_4 deposited with the ATCC under accession number 98196. In further preferred embodiments, the present invention



provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:11 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:11, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:11 having biological activity, the fragment comprising the amino acid sequence from amino acid 238 to amino acid 247 of SEQ ID NO:11.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:10.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:10, but excluding the poly(A) tail at the 3' end of SEQ ID NO:10; and

(ab) the nucleotide sequence of the cDNA insert of clone BL187\_4 deposited with the ATCC under accession number 98196;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:10, but excluding the poly(A) tail at the 3' end of SEQ ID NO:10; and

(bb) the nucleotide sequence of the cDNA insert of clone BL187\_4 deposited with the ATCC under accession number 98196;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:10, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:10 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:10, but excluding the poly(A) tail at the 3' end of SEQ ID NO:10. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:10 from nucleotide 302 to nucleotide 1762, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:10 from nucleotide 302 to nucleotide 1762, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:10 from nucleotide 302 to nucleotide 1762. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:10 from nucleotide 389 to nucleotide 1762, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:10 from nucleotide 389 to nucleotide 1762, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:10 from nucleotide 389 to nucleotide 1762. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:10 from nucleotide 1723 to nucleotide 2050, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:10 from nucleotide 1723 to nucleotide 2050, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:10 from nucleotide 1723 to nucleotide 2050.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:11;
- (b) a fragment of the amino acid sequence of SEQ ID NO:11, the fragment comprising eight contiguous amino acids of SEQ ID NO:11; and
- (c) the amino acid sequence encoded by the cDNA insert of clone BL187\_4 deposited with the ATCC under accession number 98196;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:11. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:11 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:11, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:11 having biological activity, the fragment comprising the amino acid sequence from amino acid 238 to amino acid 247 of SEQ ID NO:11.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:12;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:12  
5 from nucleotide 2 to nucleotide 2290;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:12  
from nucleotide 134 to nucleotide 2290;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:12  
from nucleotide 1 to nucleotide 309;
- 10 (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BL249\_18 deposited with the ATCC under accession number 98196;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BL249\_18 deposited with the ATCC under accession number 98196;
- 15 (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BL249\_18 deposited with the ATCC under accession number 98196;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BL249\_18 deposited with the ATCC under accession number 98196;
- 20 (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:13;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:13 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:13;
- 25 (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- (m) a polynucleotide that hybridizes under stringent conditions to any one of  
30 the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:12.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:12  
35 from nucleotide 2 to nucleotide 2290; the nucleotide sequence of SEQ ID NO:12 from nucleotide

134 to nucleotide 2290; the nucleotide sequence of SEQ ID NO:12 from nucleotide 1 to nucleotide 309; the nucleotide sequence of the full-length protein coding sequence of clone BL249\_18 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone BL249\_18 deposited with the ATCC under  
5 accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BL249\_18 deposited with the ATCC under accession number 98196. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:13 from amino acid 3 to amino acid 102. In further preferred embodiments, the present  
10 invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:13 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:13, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:13 having biological activity, the fragment comprising the amino acid sequence from amino  
15 acid 376 to amino acid 385 of SEQ ID NO:13.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:12.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 20 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:12, but excluding the poly(A) tail at the 3'  
25 end of SEQ ID NO:12; and
    - (ab) the nucleotide sequence of the cDNA insert of clone BL249\_18 deposited with the ATCC under accession number 98196;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - 30 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group  
35 consisting of:

- (ba) SEQ ID NO:12, but excluding the poly(A) tail at the 3' end of SEQ ID NO:12; and
- (bb) the nucleotide sequence of the cDNA insert of clone BL249\_18 deposited with the ATCC under accession number 98196;
- 5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide

10 sequence corresponding to the cDNA sequence of SEQ ID NO:12, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:12 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:12, but excluding the poly(A) tail at the 3' end of SEQ ID NO:12. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:12 from nucleotide

15 2 to nucleotide 2290, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:12 from nucleotide 2 to nucleotide 2290, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:12 from nucleotide 2 to nucleotide 2290. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID

20 NO:12 from nucleotide 134 to nucleotide 2290, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:12 from nucleotide 134 to nucleotide 2290, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:12 from nucleotide 134 to nucleotide 2290. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA

25 sequence of SEQ ID NO:12 from nucleotide 1 to nucleotide 309, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:12 from nucleotide 1 to nucleotide 309, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:12 from nucleotide 1 to nucleotide 309.

In other embodiments, the present invention provides a composition comprising a protein,

30 wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:13;

(b) the amino acid sequence of SEQ ID NO:13 from amino acid 3 to amino acid 102;

(c) a fragment of the amino acid sequence of SEQ ID NO:13, the fragment

35 comprising eight contiguous amino acids of SEQ ID NO:13; and

(d) the amino acid sequence encoded by the cDNA insert of clone BL249\_18 deposited with the ATCC under accession number 98196;  
the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:13 or the amino acid sequence of SEQ ID NO:13 from amino acid 3 to amino acid 102. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:13 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:13, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:13 having biological activity, the fragment comprising the amino acid sequence from amino acid 376 to amino acid 385 of SEQ ID NO:13.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 459 to nucleotide 539;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BO71\_1 deposited with the ATCC under accession number 98196;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BO71\_1 deposited with the ATCC under accession number 98196;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BO71\_1 deposited with the ATCC under accession number 98196;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BO71\_1 deposited with the ATCC under accession number 98196;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:16;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:16;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:15.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:15 from nucleotide 459 to nucleotide 539; the nucleotide sequence of the full-length protein coding sequence of clone BO71\_1 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone BO71\_1 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BO71\_1 deposited with the ATCC under accession number 98196. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 8 to amino acid 17 of SEQ ID NO:16.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:15, SEQ ID NO:14, and SEQ ID NO:17.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:  
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:14;  
(ab) SEQ ID NO:15;  
(ac) SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17; and

(ad) the nucleotide sequence of the cDNA insert of clone BO71\_1 deposited with the ATCC under accession number 98196;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:14;

(bb) SEQ ID NO:15;

(bc) SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17; and

(bd) the nucleotide sequence of the cDNA insert of clone BO71\_1 deposited with the ATCC under accession number 98196;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:14, SEQ ID NO:15, and SEQ ID NO:17, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:14 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:15 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:15. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15 from nucleotide 459 to nucleotide 539, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:15 from nucleotide 459 to nucleotide 539, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:15 from nucleotide 459 to nucleotide 539.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:16;

(b) a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16; and



- (c) the amino acid sequence encoded by the cDNA insert of clone BO71\_1 deposited with the ATCC under accession number 98196;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:16. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 8 to amino acid 17 of SEQ ID NO:16.
- 10 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:
- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:18;
  - (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:18 from nucleotide 1237 to nucleotide 1944;
  - 15 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:18 from nucleotide 737 to nucleotide 1072;
  - (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BO365\_2 deposited with the ATCC under accession number 98196;
  - 20 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BO365\_2 deposited with the ATCC under accession number 98196;
  - (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BO365\_2 deposited with the ATCC under accession number 98196;
  - 25 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BO365\_2 deposited with the ATCC under accession number 98196;
  - (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:19;
  - (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:19 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:19;
  - 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
  - (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
  - 35

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:18.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:18 from nucleotide 1237 to nucleotide 1944; the nucleotide sequence of SEQ ID NO:18 from nucleotide 737 to nucleotide 1072; the nucleotide sequence of the full-length protein coding sequence of clone BO365\_2 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone BO365\_2 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BO365\_2 deposited with the ATCC under accession number 98196. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:19 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:19, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:19 having biological activity, the fragment comprising the amino acid sequence from amino acid 113 to amino acid 122 of SEQ ID NO:19.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:18.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:18, but excluding the poly(A) tail at the 3' end of SEQ ID NO:18; and

(ab) the nucleotide sequence of the cDNA insert of clone BO365\_2 deposited with the ATCC under accession number 98196;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:  
(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:18, but excluding the poly(A) tail at the 3' end of SEQ ID NO:18; and

(bb) the nucleotide sequence of the cDNA insert of clone BO365\_2 deposited with the ATCC under accession number 98196;

10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:18, and extending contiguously  
15 from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:18 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:18, but excluding the poly(A) tail at the 3' end of SEQ ID NO:18. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:18 from nucleotide 1237 to nucleotide 1944, and extending contiguously from a nucleotide sequence corresponding  
20 to the 5' end of said sequence of SEQ ID NO:18 from nucleotide 1237 to nucleotide 1944, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:18 from nucleotide 1237 to nucleotide 1944. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:18 from nucleotide 737 to nucleotide 1072, and extending contiguously from a nucleotide  
25 sequence corresponding to the 5' end of said sequence of SEQ ID NO:18 from nucleotide 737 to nucleotide 1072, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:18 from nucleotide 737 to nucleotide 1072.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

30 (a) the amino acid sequence of SEQ ID NO:19;

(b) a fragment of the amino acid sequence of SEQ ID NO:19, the fragment comprising eight contiguous amino acids of SEQ ID NO:19; and

(c) the amino acid sequence encoded by the cDNA insert of clone BO365\_2 deposited with the ATCC under accession number 98196;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:19. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:19 having biological activity, the fragment preferably comprising eight (more preferably  
5 twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:19, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:19 having biological activity, the fragment comprising the amino acid sequence from amino acid 113 to amino acid 122 of SEQ ID NO:19.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:20;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:20 from nucleotide 68 to nucleotide 328;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BV51\_1 deposited with the ATCC under accession  
15 number 98196;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BV51\_1 deposited with the ATCC under accession number 98196;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BV51\_1 deposited with the ATCC under accession number  
20 98196;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BV51\_1 deposited with the ATCC under accession number 98196;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:21;
- 25 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:21 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:21;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 30 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:20.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:20  
5 from nucleotide 68 to nucleotide 328; the nucleotide sequence of the full-length protein coding sequence of clone BV51\_1 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone BV51\_1 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BV51\_1  
10 deposited with the ATCC under accession number 98196. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:21 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:21, or a polynucleotide encoding a protein comprising a fragment of the amino acid  
15 sequence of SEQ ID NO:21 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:21.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:20 and SEQ ID NO:22.

Further embodiments of the invention provide isolated polynucleotides produced  
20 according to a process selected from the group consisting of:

(a) a process comprising the steps of:  
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (aa) SEQ ID NO:20;  
(ab) SEQ ID NO:22, but excluding the poly(A) tail at the 3' end of SEQ ID NO:22; and  
(ac) the nucleotide sequence of the cDNA insert of clone BV51\_1 deposited with the ATCC under accession number 98196;  
30 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and  
(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:20;

5 (bb) SEQ ID NO:22, but excluding the poly(A) tail at the 3' end of SEQ ID NO:22; and

(bc) the nucleotide sequence of the cDNA insert of clone BV51\_1 deposited with the ATCC under accession number 98196;

10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:20 and SEQ ID NO:22, and  
15 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:20 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:22, but excluding the poly(A) tail at the 3' end of SEQ ID NO:22. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:20, and extending contiguously from a nucleotide sequence corresponding to the 5' end of  
20 SEQ ID NO:20 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:20. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:20 from nucleotide 68 to nucleotide 328, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:20 from nucleotide 68 to nucleotide 328, to a nucleotide  
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:20 from nucleotide 68 to nucleotide 328.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:21;

30 (b) a fragment of the amino acid sequence of SEQ ID NO:21, the fragment comprising eight contiguous amino acids of SEQ ID NO:21; and

(c) the amino acid sequence encoded by the cDNA insert of clone BV51\_1 deposited with the ATCC under accession number 98196;

the protein being substantially free from other mammalian proteins. Preferably such protein  
35 comprises the amino acid sequence of SEQ ID NO:21. In further preferred embodiments, the

present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:21 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:21, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:21 having biological activity, the fragment  
5 comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:21.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:24;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:24  
10 from nucleotide 57 to nucleotide 396;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BV140\_3 deposited with the ATCC under accession number 98196;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA  
15 insert of clone BV140\_3 deposited with the ATCC under accession number 98196;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BV140\_3 deposited with the ATCC under accession number 98196;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert  
20 of clone BV140\_3 deposited with the ATCC under accession number 98196;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:25;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:25 having biological activity, the fragment comprising eight  
25 contiguous amino acids of SEQ ID NO:25;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of  
30 the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:24.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:24 from nucleotide 57 to nucleotide 396; the nucleotide sequence of the full-length protein coding sequence of clone BV140\_3 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone BV140\_3 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BV140\_3 deposited with the ATCC under accession number 98196. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:25 from amino acid 29 to amino acid 57. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:25 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:25, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:25 having biological activity, the fragment comprising the amino acid sequence from amino acid 51 to amino acid 60 of SEQ ID NO:25.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:24, SEQ ID NO:23, and SEQ ID NO:26.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 20 (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:23;
    - 25 (ab) SEQ ID NO:24;
    - (ac) SEQ ID NO:26, but excluding the poly(A) tail at the 3' end of SEQ ID NO:26; and
    - (ad) the nucleotide sequence of the cDNA insert of clone BV140\_3 deposited with the ATCC under accession number 98196;
  - 30 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:



(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (ba) SEQ ID NO:23;
- 5 (bb) SEQ ID NO:24;
- (bc) SEQ ID NO:26, but excluding the poly(A) tail at the 3' end of SEQ ID NO:26; and
- (bd) the nucleotide sequence of the cDNA insert of clone BV140\_3 deposited with the ATCC under accession number 98196;
- 10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide  
15 sequence corresponding to the cDNA sequences of SEQ ID NO:23, SEQ ID NO:24, and SEQ ID NO:26, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:23 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:26, but excluding the poly(A) tail at the 3' end of SEQ ID NO:26. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the  
20 cDNA sequence of SEQ ID NO:24, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:24 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:24. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:24 from nucleotide 57 to nucleotide 396, and extending contiguously from a nucleotide sequence  
25 corresponding to the 5' end of said sequence of SEQ ID NO:24 from nucleotide 57 to nucleotide 396, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:24 from nucleotide 57 to nucleotide 396.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 30 (a) the amino acid sequence of SEQ ID NO:25;
- (b) the amino acid sequence of SEQ ID NO:25 from amino acid 29 to amino acid 57;
- (c) a fragment of the amino acid sequence of SEQ ID NO:25, the fragment comprising eight contiguous amino acids of SEQ ID NO:25; and

(d) the amino acid sequence encoded by the cDNA insert of clone BV140\_3 deposited with the ATCC under accession number 98196; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:25 or the amino acid sequence of SEQ ID NO:25 from amino acid 29 to amino acid 57. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:25 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:25, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:25 having biological activity, the fragment comprising the amino acid sequence from amino acid 51 to amino acid 60 of SEQ ID NO:25.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 101 to nucleotide 328;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 1 to nucleotide 197;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BV141\_2 deposited with the ATCC under accession number 98196;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BV141\_2 deposited with the ATCC under accession number 98196;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BV141\_2 deposited with the ATCC under accession number 98196;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BV141\_2 deposited with the ATCC under accession number 98196;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:28;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:28;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

5 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:27.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:27 from nucleotide 101 to nucleotide 328; the nucleotide sequence of SEQ ID NO:27 from  
10 nucleotide 1 to nucleotide 197; the nucleotide sequence of the full-length protein coding sequence of clone BV141\_2 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone BV141\_2 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BV141\_2 deposited with the  
15 ATCC under accession number 98196. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:28 from amino acid 1 to amino acid 37. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably comprising eight  
20 (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:28, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 33 to amino acid 42 of SEQ ID NO:28.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID  
25 NO:27.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X  
30 SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and

(ab) the nucleotide sequence of the cDNA insert of clone  
35 BV141\_2 deposited with the ATCC under accession number 98196;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

5 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and

(bb) the nucleotide sequence of the cDNA insert of clone BV141\_2 deposited with the ATCC under accession number 98196;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

15 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:27 to a nucleotide sequence  
20 corresponding to the 3' end of SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27 from nucleotide 101 to nucleotide 328, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:27 from nucleotide 101 to nucleotide 328, to a  
25 nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:27 from nucleotide 101 to nucleotide 328. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27 from nucleotide 1 to nucleotide 197, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:27 from nucleotide 1 to  
30 nucleotide 197, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:27 from nucleotide 1 to nucleotide 197.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:28;

(b) the amino acid sequence of SEQ ID NO:28 from amino acid 1 to amino acid 37;

(c) a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28; and

5 (d) the amino acid sequence encoded by the cDNA insert of clone BV141\_2 deposited with the ATCC under accession number 98196;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:28 or the amino acid sequence of SEQ ID NO:28 from amino acid 1 to amino acid 37. In further preferred embodiments, the present  
10 invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:28, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 33 to amino acid 42 of SEQ ID NO:28.

15 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29 from nucleotide 28 to nucleotide 351;

20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29 from nucleotide 328 to nucleotide 351;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CC194\_4 deposited with the ATCC under accession number 98196;

25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CC194\_4 deposited with the ATCC under accession number 98196;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CC194\_4 deposited with the ATCC under accession number 98196;

30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CC194\_4 deposited with the ATCC under accession number 98196;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:30;

- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:30;
- 5 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 10 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:29.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:29 from nucleotide 28 to nucleotide 351; the nucleotide sequence of SEQ ID NO:29 from nucleotide 15 328 to nucleotide 351; the nucleotide sequence of the full-length protein coding sequence of clone CC194\_4 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone CC194\_4 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CC194\_4 deposited with the ATCC under 20 accession number 98196. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:30 from amino acid 56 to amino acid 108. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more 25 preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:30, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 49 to amino acid 58 of SEQ ID NO:30.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID 30 NO:29 and SEQ ID NO:31.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:29;

5 (ab) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and

(ac) the nucleotide sequence of the cDNA insert of clone CC194\_4 deposited with the ATCC under accession number 98196;

10 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:29;

(bb) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and

20 (bc) the nucleotide sequence of the cDNA insert of clone CC194\_4 deposited with the ATCC under accession number 98196;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

25 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:29 and SEQ ID NO:31, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:29 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:29 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:29. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29 from nucleotide 28 to

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nucleotide 351, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:29 from nucleotide 28 to nucleotide 351, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:29 from nucleotide 28 to nucleotide 351. Also preferably the polynucleotide isolated according to the above process

5 comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29 from nucleotide 328 to nucleotide 351, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:29 from nucleotide 328 to nucleotide 351, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:29 from nucleotide 328 to nucleotide 351.

10 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:30;
- (b) the amino acid sequence of SEQ ID NO:30 from amino acid 56 to amino acid 108;
- 15 (c) a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CC194\_4 deposited with the ATCC under accession number 98196;

the protein being substantially free from other mammalian proteins. Preferably such protein

20 comprises the amino acid sequence of SEQ ID NO:30 or the amino acid sequence of SEQ ID NO:30 from amino acid 56 to amino acid 108. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:30, or a protein comprising a

25 fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 49 to amino acid 58 of SEQ ID NO:30.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:32;
- 30 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:32 from nucleotide 338 to nucleotide 1198;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:32 from nucleotide 467 to nucleotide 1058;



- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone DA136\_11 deposited with the ATCC under accession number 98196;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone DA136\_11 deposited with the ATCC under accession number 98196;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone DA136\_11 deposited with the ATCC under accession number 98196;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone DA136\_11 deposited with the ATCC under accession number 98196;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:33;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:33 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:33;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:32.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:32 from nucleotide 338 to nucleotide 1198; the nucleotide sequence of SEQ ID NO:32 from nucleotide 467 to nucleotide 1058; the nucleotide sequence of the full-length protein coding sequence of clone DA136\_11 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone DA136\_11 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone DA136\_11 deposited with the ATCC under accession number 98196. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:33 from amino acid 124 to amino acid 182. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a

fragment of the amino acid sequence of SEQ ID NO:33 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:33, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:33 having biological activity, the fragment comprising the amino acid sequence from amino acid 138 to amino acid 147 of SEQ ID NO:33.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:32.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 10 (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 15 (aa) SEQ ID NO:32, but excluding the poly(A) tail at the 3' end of SEQ ID NO:32; and
    - (ab) the nucleotide sequence of the cDNA insert of clone DA136\_11 deposited with the ATCC under accession number 98196;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - 20 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 25 (ba) SEQ ID NO:32, but excluding the poly(A) tail at the 3' end of SEQ ID NO:32; and
    - (bb) the nucleotide sequence of the cDNA insert of clone DA136\_11 deposited with the ATCC under accession number 98196;
    - 30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
    - (iii) amplifying human DNA sequences; and
    - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:32, and extending contiguously

from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:32 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:32, but excluding the poly(A) tail at the 3' end of SEQ ID NO:32. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:32 from nucleotide 338 to nucleotide 1198, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:32 from nucleotide 338 to nucleotide 1198, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:32 from nucleotide 338 to nucleotide 1198. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:32 from nucleotide 467 to nucleotide 1058, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:32 from nucleotide 467 to nucleotide 1058, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:32 from nucleotide 467 to nucleotide 1058.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:33;
- (b) the amino acid sequence of SEQ ID NO:33 from amino acid 124 to amino acid 182;
- (c) a fragment of the amino acid sequence of SEQ ID NO:33, the fragment comprising eight contiguous amino acids of SEQ ID NO:33; and
- (d) the amino acid sequence encoded by the cDNA insert of clone DA136\_11 deposited with the ATCC under accession number 98196;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:33 or the amino acid sequence of SEQ ID NO:33 from amino acid 124 to amino acid 182. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:33 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:33, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:33 having biological activity, the fragment comprising the amino acid sequence from amino acid 138 to amino acid 147 of SEQ ID NO:33.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:34;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:34 from nucleotide 437 to nucleotide 1159;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:34 from nucleotide 515 to nucleotide 1159;
- 5 (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:34 from nucleotide 539 to nucleotide 1099;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AR415\_4 deposited with the ATCC under accession number 98232;
- 10 (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AR415\_4 deposited with the ATCC under accession number 98232;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AR415\_4 deposited with the ATCC under accession number 98232;
- 15 (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AR415\_4 deposited with the ATCC under accession number 98232;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:35;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:35 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:35;
- 20 (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- 25 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:34.
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Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:34 from nucleotide 437 to nucleotide 1159; the nucleotide sequence of SEQ ID NO:34 from nucleotide 515 to nucleotide 1159; the nucleotide sequence of SEQ ID NO:34 from nucleotide 539 to nucleotide 1099; the nucleotide sequence of the full-length protein coding sequence of clone AR415\_4 deposited with the ATCC under accession number 98232; or the nucleotide

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sequence of a mature protein coding sequence of clone AR415\_4 deposited with the ATCC under accession number 98232. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AR415\_4 deposited with the ATCC under accession number 98232. In yet other preferred embodiments, the present invention  
5 provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:35 from amino acid 51 to amino acid 221. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:35 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:35, or a  
10 polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:35 having biological activity, the fragment comprising the amino acid sequence from amino acid 115 to amino acid 124 of SEQ ID NO:35.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:34.

15 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:  
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- (aa) SEQ ID NO:34, but excluding the poly(A) tail at the 3' end of SEQ ID NO:34; and

- (ab) the nucleotide sequence of the cDNA insert of clone AR415\_4 deposited with the ATCC under accession number 98232;

- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

- (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:

- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:  
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- (ba) SEQ ID NO:34, but excluding the poly(A) tail at the 3' end of SEQ ID NO:34; and

- (bb) the nucleotide sequence of the cDNA insert of clone AR415\_4 deposited with the ATCC under accession number 98232;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:34, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:34 to a nucleotide sequence  
10 corresponding to the 3' end of SEQ ID NO:34, but excluding the poly(A) tail at the 3' end of SEQ ID NO:34. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:34 from nucleotide 437 to nucleotide 1159, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:34 from nucleotide 437 to nucleotide 1159, to a  
15 nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:34 from nucleotide 437 to nucleotide 1159. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:34 from nucleotide 515 to nucleotide 1159, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:34 from nucleotide 515 to  
20 nucleotide 1159, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:34 from nucleotide 515 to nucleotide 1159. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:34 from nucleotide 539 to nucleotide 1099, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:34 from  
25 nucleotide 539 to nucleotide 1099, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:34 from nucleotide 539 to nucleotide 1099.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:35;
- 30 (b) the amino acid sequence of SEQ ID NO:35 from amino acid 51 to amino acid 221;
- (c) a fragment of the amino acid sequence of SEQ ID NO:35, the fragment comprising eight contiguous amino acids of SEQ ID NO:35; and
- (d) the amino acid sequence encoded by the cDNA insert of clone AR415\_4  
35 deposited with the ATCC under accession number 98232;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:35 or the amino acid sequence of SEQ ID NO:35 from amino acid 51 to amino acid 221. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:35 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:35, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:35 having biological activity, the fragment comprising the amino acid sequence from amino acid 115 to amino acid 124 of SEQ ID NO:35.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:36;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:36 from nucleotide 59 to nucleotide 376;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:36 from nucleotide 179 to nucleotide 376;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AS63\_29 deposited with the ATCC under accession number 98232;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AS63\_29 deposited with the ATCC under accession number 98232;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AS63\_29 deposited with the ATCC under accession number 98232;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AS63\_29 deposited with the ATCC under accession number 98232;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:37;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:37 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:37;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:36.

5 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:36 from nucleotide 59 to nucleotide 376; the nucleotide sequence of SEQ ID NO:36 from nucleotide 179 to nucleotide 376; the nucleotide sequence of the full-length protein coding sequence of clone AS63\_29 deposited with the ATCC under accession number 98232; or the nucleotide sequence  
10 of a mature protein coding sequence of clone AS63\_29 deposited with the ATCC under accession number 98232. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AS63\_29 deposited with the ATCC under accession number 98232. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:37 from  
15 amino acid 1 to amino acid 91. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:37 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:37, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:37 having  
20 biological activity, the fragment comprising the amino acid sequence from amino acid 48 to amino acid 57 of SEQ ID NO:37.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:36 and SEQ ID NO:38.

Further embodiments of the invention provide isolated polynucleotides produced  
25 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (aa) SEQ ID NO:36;  
(ab) SEQ ID NO:38, but excluding the poly(A) tail at the 3' end of SEQ ID NO:38; and  
(ac) the nucleotide sequence of the cDNA insert of clone AS63\_29 deposited with the ATCC under accession number 98232;



(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

5 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:36;

10 (bb) SEQ ID NO:38, but excluding the poly(A) tail at the 3' end of SEQ ID NO:38; and

(bc) the nucleotide sequence of the cDNA insert of clone AS63\_29 deposited with the ATCC under accession number 98232;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

15 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:36 and SEQ ID NO:38, and  
 20 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:36 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:38, but excluding the poly(A) tail at the 3' end of SEQ ID NO:38. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:36, and extending contiguously from a nucleotide sequence corresponding to the 5' end of  
 25 SEQ ID NO:36 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:36. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:36 from nucleotide 59 to nucleotide 376, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:36 from nucleotide 59 to nucleotide 376, to a nucleotide  
 30 sequence corresponding to the 3' end of said sequence of SEQ ID NO:36 from nucleotide 59 to nucleotide 376. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:36 from nucleotide 179 to nucleotide 376, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:36 from nucleotide 179 to nucleotide

376, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:36 from nucleotide 179 to nucleotide 376.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 5                   (a)     the amino acid sequence of SEQ ID NO:37;
- (b)     the amino acid sequence of SEQ ID NO:37 from amino acid 1 to amino acid 91;
- (c)     a fragment of the amino acid sequence of SEQ ID NO:37, the fragment comprising eight contiguous amino acids of SEQ ID NO:37; and
- 10                  (d)     the amino acid sequence encoded by the cDNA insert of clone AS63\_29 deposited with the ATCC under accession number 98232;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:37 or the amino acid sequence of SEQ ID NO:37 from amino acid 1 to amino acid 91. In further preferred embodiments, the present  
15 invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:37 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:37, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:37 having biological activity, the fragment comprising the amino acid sequence from amino acid 48 to amino acid 57 of SEQ ID NO:37.

20                  In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39;
- (b)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39 from nucleotide 198 to nucleotide 2039;
- 25                  (c)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39 from nucleotide 490 to nucleotide 809;
- (d)     a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AY304\_14 deposited with the ATCC under accession number 98561;
- 30                  (e)     a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AY304\_14 deposited with the ATCC under accession number 98561;
- (f)     a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AY304\_14 deposited with the ATCC under accession number 98561;

- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AY304\_14 deposited with the ATCC under accession number 98561;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:40;
- 5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:40;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of
- 15 the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:39.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:39 from nucleotide 198 to nucleotide 2039; the nucleotide sequence of SEQ ID NO:39 from nucleotide 490 to nucleotide 809; the nucleotide sequence of the full-length protein coding

20 sequence of clone AY304\_14 deposited with the ATCC under accession number 98561; or the nucleotide sequence of a mature protein coding sequence of clone AY304\_14 deposited with the ATCC under accession number 98561. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AY304\_14 deposited with the ATCC under accession number 98561. In yet other preferred embodiments,

25 the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:40 from amino acid 106 to amino acid 204. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino

30 acids of SEQ ID NO:40, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 302 to amino acid 311 of SEQ ID NO:40.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:39.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and
    - (ab) the nucleotide sequence of the cDNA insert of clone AY304\_14 deposited with the ATCC under accession number 98561;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and
    - (bb) the nucleotide sequence of the cDNA insert of clone AY304\_14 deposited with the ATCC under accession number 98561;
  - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
  - (iii) amplifying human DNA sequences; and
  - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:39 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39 from nucleotide 198 to nucleotide 2039, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:39 from nucleotide 198 to nucleotide 2039, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:39 from

nucleotide 198 to nucleotide 2039. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39 from nucleotide 490 to nucleotide 809, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:39 from nucleotide 490 to  
 5 nucleotide 809, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:39 from nucleotide 490 to nucleotide 809.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:40;
- 10 (b) the amino acid sequence of SEQ ID NO:40 from amino acid 106 to amino acid 204;
- (c) a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40; and
- (d) the amino acid sequence encoded by the cDNA insert of clone AY304\_14  
 15 deposited with the ATCC under accession number 98561;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:40 or the amino acid sequence of SEQ ID NO:40 from amino acid 106 to amino acid 204. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40  
 20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:40, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 302 to amino acid 311 of SEQ ID NO:40.

25 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41  
 from nucleotide 102 to nucleotide 2027;
- 30 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41  
 from nucleotide 1902 to nucleotide 2027;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41  
 from nucleotide 1 to nucleotide 431;

- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BG160\_1 deposited with the ATCC under accession number 98232;
- 5 (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BG160\_1 deposited with the ATCC under accession number 98232;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BG160\_1 deposited with the ATCC under accession number 98232;
- 10 (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BG160\_1 deposited with the ATCC under accession number 98232;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:42;
- 15 (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:42;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- 20 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:41.
- 25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:41 from nucleotide 102 to nucleotide 2027; the nucleotide sequence of SEQ ID NO:41 from nucleotide 1902 to nucleotide 2027; the nucleotide sequence of SEQ ID NO:41 from nucleotide 1 to nucleotide 431; the nucleotide sequence of the full-length protein coding sequence of clone BG160\_1 deposited with the ATCC under accession number 98232; or the nucleotide sequence
- 30 of a mature protein coding sequence of clone BG160\_1 deposited with the ATCC under accession number 98232. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BG160\_1 deposited with the ATCC under accession number 98232. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:42 from
- 35 amino acid 1 to amino acid 110. In further preferred embodiments, the present invention provides

a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:42, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having  
5 biological activity, the fragment comprising the amino acid sequence from amino acid 316 to amino acid 325 of SEQ ID NO:42.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:41.

Further embodiments of the invention provide isolated polynucleotides produced  
10 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

15 (aa) SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41; and

(ab) the nucleotide sequence of the cDNA insert of clone BG160\_1 deposited with the ATCC under accession number 98232;

(ii) hybridizing said probe(s) to human genomic DNA in conditions  
20 at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in  
25 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41; and

30 (bb) the nucleotide sequence of the cDNA insert of clone BG160\_1 deposited with the ATCC under accession number 98232;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:41 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 102 to nucleotide 207, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 102 to nucleotide 207, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 102 to nucleotide 207. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 1902 to nucleotide 207, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 1902 to nucleotide 207, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 1902 to nucleotide 207. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 1 to nucleotide 431, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 1 to nucleotide 431, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 1 to nucleotide 431.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:42;
- (b) the amino acid sequence of SEQ ID NO:42 from amino acid 1 to amino acid 110;
- (c) a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42; and
- (d) the amino acid sequence encoded by the cDNA insert of clone BG160\_1 deposited with the ATCC under accession number 98232;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:42 or the amino acid sequence of SEQ ID NO:42 from amino acid 1 to amino acid 110. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:42, or a protein comprising a



fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising the amino acid sequence from amino acid 316 to amino acid 325 of SEQ ID NO:42.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5                   (a)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:44;
- (b)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:44 from nucleotide 566 to nucleotide 631;
- (c)     a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BO432\_4 deposited with the ATCC under accession number 98232;
- 10                  (d)     a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BO432\_4 deposited with the ATCC under accession number 98232;
- (e)     a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BO432\_4 deposited with the ATCC under accession number 98232;
- 15                  (f)     a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BO432\_4 deposited with the ATCC under accession number 98232;
- (g)     a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:45;
- 20                  (h)     a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:45 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:45;
- (i)     a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 25                  (j)     a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k)     a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l)     a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:44.
- 30

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:44 from nucleotide 566 to nucleotide 631; the nucleotide sequence of the full-length protein coding sequence of clone BO432\_4 deposited with the ATCC under accession number 98232; or the  
35   nucleotide sequence of a mature protein coding sequence of clone BO432\_4 deposited with the

ATCC under accession number 98232. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BO432\_4 deposited with the ATCC under accession number 98232. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:45 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:45, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:45 having biological activity, the fragment comprising the amino acid sequence from amino acid 6 to amino acid 15 of SEQ ID NO:45.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:44, SEQ ID NO:43, and SEQ ID NO:46.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:43;
    - (ab) SEQ ID NO:44;
    - (ac) SEQ ID NO:46, but excluding the poly(A) tail at the 3' end of SEQ ID NO:46; and
    - (ad) the nucleotide sequence of the cDNA insert of clone BO432\_4 deposited with the ATCC under accession number 98232;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:43;
    - (bb) SEQ ID NO:44;
    - (bc) SEQ ID NO:46, but excluding the poly(A) tail at the 3' end of SEQ ID NO:46; and

- (bd) the nucleotide sequence of the cDNA insert of clone BO432\_4 deposited with the ATCC under accession number 98232;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:43, SEQ ID NO:44, and SEQ ID NO:46, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:43 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:46, but excluding the poly(A) tail at the 3' end of SEQ ID NO:46. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:44, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:44 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:44. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:44 from nucleotide 566 to nucleotide 631, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:44 from nucleotide 566 to nucleotide 631, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:44 from nucleotide 566 to nucleotide 631.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:45;
- (b) a fragment of the amino acid sequence of SEQ ID NO:45, the fragment comprising eight contiguous amino acids of SEQ ID NO:45; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone BO432\_4 deposited with the ATCC under accession number 98232;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:45. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:45 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:45, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:45 having biological activity, the fragment comprising the amino acid sequence from amino acid 6 to amino acid 15 of SEQ ID NO:45.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47  
5 from nucleotide 45 to nucleotide 428;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BO538\_2 deposited with the ATCC under accession number 98232;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA  
10 insert of clone BO538\_2 deposited with the ATCC under accession number 98232;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BO538\_2 deposited with the ATCC under accession number 98232;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert  
15 of clone BO538\_2 deposited with the ATCC under accession number 98232;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:48;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising eight  
20 contiguous amino acids of SEQ ID NO:48;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of  
25 the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:47.

30 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:47 from nucleotide 45 to nucleotide 428; the nucleotide sequence of the full-length protein coding sequence of clone BO538\_2 deposited with the ATCC under accession number 98232; or the nucleotide sequence of a mature protein coding sequence of clone BO538\_2 deposited with the ATCC under accession number 98232. In other preferred embodiments, the polynucleotide  
35 encodes the full-length or a mature protein encoded by the cDNA insert of clone BO538\_2

deposited with the ATCC under accession number 98232. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:48 from amino acid 52 to amino acid 128. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a  
5 fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:48, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising the amino acid sequence from amino acid 59 to amino acid 68 of SEQ ID NO:48.

10 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:47 and SEQ ID NO:49.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - 15 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:47;
    - (ab) SEQ ID NO:49, but excluding the poly(A) tail at the 3'  
20 end of SEQ ID NO:49; and
    - (ac) the nucleotide sequence of the cDNA insert of clone BO538\_2 deposited with the ATCC under accession number 98232;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - 25 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
    - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group  
30 consisting of:
      - (ba) SEQ ID NO:47;
      - (bb) SEQ ID NO:49, but excluding the poly(A) tail at the 3'  
end of SEQ ID NO:49; and
      - (bc) the nucleotide sequence of the cDNA insert of clone BO538\_2 deposited with the ATCC under accession number 98232;
- 35

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
  - (iii) amplifying human DNA sequences; and
  - (iv) isolating the polynucleotide products of step (b)(iii).
- 5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:47 and SEQ ID NO:49, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:47 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49. Also preferably the polynucleotide isolated according to the
- 10 above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:47 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:47. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47 from nucleotide 45 to
- 15 nucleotide 428, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from nucleotide 45 to nucleotide 428, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 45 to nucleotide 428.

- In other embodiments, the present invention provides a composition comprising a protein,
- 20 wherein said protein comprises an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:48;
  - (b) the amino acid sequence of SEQ ID NO:48 from amino acid 52 to amino acid 128;
  - (c) a fragment of the amino acid sequence of SEQ ID NO:48, the fragment
- 25 comprising eight contiguous amino acids of SEQ ID NO:48; and
- (d) the amino acid sequence encoded by the cDNA insert of clone BO538\_2 deposited with the ATCC under accession number 98232;

- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:48 or the amino acid sequence of SEQ ID
- 30 NO:48 from amino acid 52 to amino acid 128. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:48, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment
- 35 comprising the amino acid sequence from amino acid 59 to amino acid 68 of SEQ ID NO:48.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:50;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:50  
5 from nucleotide 144 to nucleotide 566;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BR595\_4 deposited with the ATCC under accession number 98232;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA  
10 insert of clone BR595\_4 deposited with the ATCC under accession number 98232;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BR595\_4 deposited with the ATCC under accession number 98232;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert  
15 of clone BR595\_4 deposited with the ATCC under accession number 98232;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:51;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:51 having biological activity, the fragment comprising eight  
20 contiguous amino acids of SEQ ID NO:51;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of  
25 the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:50.

30 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:50 from nucleotide 144 to nucleotide 566; the nucleotide sequence of the full-length protein coding sequence of clone BR595\_4 deposited with the ATCC under accession number 98232; or the nucleotide sequence of a mature protein coding sequence of clone BR595\_4 deposited with the ATCC under accession number 98232. In other preferred embodiments, the polynucleotide  
35 encodes the full-length or a mature protein encoded by the cDNA insert of clone BR595\_4

deposited with the ATCC under accession number 98232. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:51 from amino acid 39 to amino acid 141. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a  
5 fragment of the amino acid sequence of SEQ ID NO:51 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:51, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:51 having biological activity, the fragment comprising the amino acid sequence from amino acid 65 to amino acid 74 of SEQ ID NO:51.

10 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:50 and SEQ ID NO:52.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - 15 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:50;
    - (ab) SEQ ID NO:52, but excluding the poly(A) tail at the 3'  
20 end of SEQ ID NO:52; and
    - (ac) the nucleotide sequence of the cDNA insert of clone BR595\_4 deposited with the ATCC under accession number 98232;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - 25 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in  
30 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:50;
    - (bb) SEQ ID NO:52, but excluding the poly(A) tail at the 3'  
end of SEQ ID NO:52; and
    - (bc) the nucleotide sequence of the cDNA insert of clone  
35 BR595\_4 deposited with the ATCC under accession number 98232;



- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
  - (iii) amplifying human DNA sequences; and
  - (iv) isolating the polynucleotide products of step (b)(iii).
- 5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:50 and SEQ ID NO:52, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:50 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:52, but excluding the poly(A) tail at the 3' end of SEQ ID NO:52. Also preferably the polynucleotide isolated according to the
- 10 above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:50, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:50 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:50. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:50 from nucleotide 144 to
- 15 nucleotide 566, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:50 from nucleotide 144 to nucleotide 566, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:50 from nucleotide 144 to nucleotide 566.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:51;
- (b) the amino acid sequence of SEQ ID NO:51 from amino acid 39 to amino acid 141;
- (c) a fragment of the amino acid sequence of SEQ ID NO:51, the fragment
- 25 comprising eight contiguous amino acids of SEQ ID NO:51; and
- (d) the amino acid sequence encoded by the cDNA insert of clone BR595\_4 deposited with the ATCC under accession number 98232;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:51 or the amino acid sequence of SEQ ID

30 NO:51 from amino acid 39 to amino acid 141. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:51 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:51, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:51 having biological activity, the fragment

35 comprising the amino acid sequence from amino acid 65 to amino acid 74 of SEQ ID NO:51.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53  
5 from nucleotide 232 to nucleotide 1041;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53  
from nucleotide 460 to nucleotide 1041;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53  
from nucleotide 590 to nucleotide 1163;
- 10 (e) a polynucleotide comprising the nucleotide sequence of the full-length  
protein coding sequence of clone CI490\_2 deposited with the ATCC under accession  
number 98232;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA  
insert of clone CI490\_2 deposited with the ATCC under accession number 98232;
- 15 (g) a polynucleotide comprising the nucleotide sequence of a mature protein  
coding sequence of clone CI490\_2 deposited with the ATCC under accession number  
98232;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert  
of clone CI490\_2 deposited with the ATCC under accession number 98232;
- 20 (i) a polynucleotide encoding a protein comprising the amino acid sequence  
of SEQ ID NO:54;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino  
acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising eight  
contiguous amino acids of SEQ ID NO:54;
- 25 (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h)  
above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i)  
or (j) above ;
- (m) a polynucleotide that hybridizes under stringent conditions to any one of  
30 the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of  
the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the  
length of SEQ ID NO:53.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:53  
35 from nucleotide 232 to nucleotide 1041; the nucleotide sequence of SEQ ID NO:53 from

nucleotide 460 to nucleotide 1041; the nucleotide sequence of SEQ ID NO:53 from nucleotide 590 to nucleotide 1163; the nucleotide sequence of the full-length protein coding sequence of clone CI490\_2 deposited with the ATCC under accession number 98232; or the nucleotide sequence of a mature protein coding sequence of clone CI490\_2 deposited with the ATCC under  
5 accession number 98232. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CI490\_2 deposited with the ATCC under accession number 98232. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:54 from amino acid 133 to amino acid 270. In further preferred embodiments, the present  
10 invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence from amino  
15 acid 130 to amino acid 139 of SEQ ID NO:54.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:53.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 20 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:53, but excluding the poly(A) tail at the 3'  
25 end of SEQ ID NO:53; and
    - (ab) the nucleotide sequence of the cDNA insert of clone CI490\_2 deposited with the ATCC under accession number 98232;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - 30 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in  
35 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53; and

(bb) the nucleotide sequence of the cDNA insert of clone CI490\_2 deposited with the ATCC under accession number 98232;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide  
10 sequence corresponding to the cDNA sequence of SEQ ID NO:53, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:53 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53 from nucleotide  
15 232 to nucleotide 1041, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from nucleotide 232 to nucleotide 1041, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide 232 to nucleotide 1041. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
20 NO:53 from nucleotide 460 to nucleotide 1041, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from nucleotide 460 to nucleotide 1041, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide 460 to nucleotide 1041. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA  
25 sequence of SEQ ID NO:53 from nucleotide 590 to nucleotide 1163, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from nucleotide 590 to nucleotide 1163, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide 590 to nucleotide 1163.

In other embodiments, the present invention provides a composition comprising a protein,  
30 wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:54;

(b) the amino acid sequence of SEQ ID NO:54 from amino acid 133 to amino acid 270;

(c) a fragment of the amino acid sequence of SEQ ID NO:54, the fragment  
35 comprising eight contiguous amino acids of SEQ ID NO:54; and

(d) the amino acid sequence encoded by the cDNA insert f clone CI490\_2 deposited with the ATCC under accession number 98232;  
the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:54 or the amino acid sequence of SEQ ID NO:54 from amino acid 133 to amino acid 270. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence from amino acid 130 to amino acid 139 of SEQ ID NO:54.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55 from nucleotide 268 to nucleotide 624;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55 from nucleotide 325 to nucleotide 624;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CI522\_1 deposited with the ATCC under accession number 98232;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CI522\_1 deposited with the ATCC under accession number 98232;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CI522\_1 deposited with the ATCC under accession number 98232;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CI522\_1 deposited with the ATCC under accession number 98232;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:56;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:56;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

5 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:55.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:55 from nucleotide 268 to nucleotide 624; the nucleotide sequence of SEQ ID NO:55 from nucleotide  
10 325 to nucleotide 624; the nucleotide sequence of the full-length protein coding sequence of clone CI522\_1 deposited with the ATCC under accession number 98232; or the nucleotide sequence of a mature protein coding sequence of clone CI522\_1 deposited with the ATCC under accession number 98232. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CI522\_1 deposited with the ATCC under  
15 accession number 98232. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:56, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having  
20 biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:56.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:55 and SEQ ID NO:57.

Further embodiments of the invention provide isolated polynucleotides produced  
25 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (aa) SEQ ID NO:55;  
(ab) SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57; and  
(ac) the nucleotide sequence of the cDNA insert of clone CI522\_1 deposited with the ATCC under accession number 98232;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

5 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:55;

10 (bb) SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57; and

(bc) the nucleotide sequence of the cDNA insert of clone CI522\_1 deposited with the ATCC under accession number 98232;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

15 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:55 and SEQ ID NO:57, and  
20 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:55 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55, and extending contiguously from a nucleotide sequence corresponding to the 5' end of  
25 SEQ ID NO:55 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:55. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55 from nucleotide 268 to nucleotide 624, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:55 from nucleotide 268 to nucleotide 624, to a nucleotide  
30 sequence corresponding to the 3' end of said sequence of SEQ ID NO:55 from nucleotide 268 to nucleotide 624. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55 from nucleotide 325 to nucleotide 624, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:55 from nucleotide 325 to nucleotide

624, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:55 from nucleotide 325 to nucleotide 624.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 5 (a) the amino acid sequence of SEQ ID NO:56;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone CI522\_1 deposited with the ATCC under accession number 98232;
- 10 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:56. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:56, or a protein comprising
- 15 a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:56.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:58;
- 20 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:58 from nucleotide 288 to nucleotide 710;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:58 from nucleotide 868 to nucleotide 1887;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CN238\_1 deposited with the ATCC under accession number 98232;
- 25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CN238\_1 deposited with the ATCC under accession number 98232;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CN238\_1 deposited with the ATCC under accession number
- 30 98232;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CN238\_1 deposited with the ATCC under accession number 98232;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence
- 35 of SEQ ID NO:59;



(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:59 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:59;

5 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

10 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:58.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:58 from nucleotide 288 to nucleotide 710; the nucleotide sequence of SEQ ID NO:58 from  
15 nucleotide 868 to nucleotide 1887; the nucleotide sequence of the full-length protein coding sequence of clone CN238\_1 deposited with the ATCC under accession number 98232; or the nucleotide sequence of a mature protein coding sequence of clone CN238\_1 deposited with the ATCC under accession number 98232. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CN238\_1  
20 deposited with the ATCC under accession number 98232. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:59 from amino acid 1 to amino acid 109. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:59 having biological activity, the fragment  
25 preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:59, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:59 having biological activity, the fragment comprising the amino acid sequence from amino acid 65 to amino acid 74 of SEQ ID NO:59.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID  
30 NO:58.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (aa) SEQ ID NO:58, but excluding the poly(A) tail at the 3' end of SEQ ID NO:58; and

(ab) the nucleotide sequence of the cDNA insert of clone CN238\_1 deposited with the ATCC under accession number 98232;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

10 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:58, but excluding the poly(A) tail at the 3' end of SEQ ID NO:58; and

(bb) the nucleotide sequence of the cDNA insert of clone CN238\_1 deposited with the ATCC under accession number 98232;

20 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide  
25 sequence corresponding to the cDNA sequence of SEQ ID NO:58, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:58 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:58, but excluding the poly(A) tail at the 3' end of SEQ ID NO:58. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:58 from nucleotide  
30 288 to nucleotide 710, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:58 from nucleotide 288 to nucleotide 710, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:58 from nucleotide 288 to nucleotide 710. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
35 NO:58 from nucleotide 868 to nucleotide 1887, and extending contiguously from a nucleotide

sequence corresponding to the 5' end of said sequence of SEQ ID NO:58 from nucleotide 868 to nucleotide 1887, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:58 from nucleotide 868 to nucleotide 1887.

In other embodiments, the present invention provides a composition comprising a protein,  
5 wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:59;
- (b) the amino acid sequence of SEQ ID NO:59 from amino acid 1 to amino acid 109;
- (c) a fragment of the amino acid sequence of SEQ ID NO:59, the fragment  
10 comprising eight contiguous amino acids of SEQ ID NO:59; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CN238\_1 deposited with the ATCC under accession number 98232;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:59 or the amino acid sequence of SEQ ID  
15 NO:59 from amino acid 1 to amino acid 109. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:59 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:59, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:59 having biological activity, the fragment  
20 comprising the amino acid sequence from amino acid 65 to amino acid 74 of SEQ ID NO:59.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:60;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:60  
25 from nucleotide 87 to nucleotide 1871;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:60 from nucleotide 628 to nucleotide 1882;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CO390\_1 deposited with the ATCC under accession  
30 number 98232;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CO390\_1 deposited with the ATCC under accession number 98232;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CO390\_1 deposited with the ATCC under accession number  
35 98232;

- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CO390\_1 deposited with the ATCC under accession number 98232;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:61;
- 5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:61 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:61;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:60.
- 15

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:60 from nucleotide 87 to nucleotide 1871; the nucleotide sequence of SEQ ID NO:60 from nucleotide 628 to nucleotide 1882; the nucleotide sequence of the full-length protein coding sequence of clone CO390\_1 deposited with the ATCC under accession number 98232; or the nucleotide sequence of a mature protein coding sequence of clone CO390\_1 deposited with the ATCC under accession number 98232. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CO390\_1 deposited with the ATCC under accession number 98232. In yet other preferred embodiments,

20 the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:61 from amino acid 182 to amino acid 248. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:61 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:61, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:61 having biological activity, the fragment comprising the amino acid sequence from amino acid 292 to amino acid 301 of SEQ ID NO:61.

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Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:60.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:60, but excluding the poly(A) tail at the 3' end of SEQ ID NO:60; and
    - (ab) the nucleotide sequence of the cDNA insert of clone CO390\_1 deposited with the ATCC under accession number 98232;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:60, but excluding the poly(A) tail at the 3' end of SEQ ID NO:60; and
    - (bb) the nucleotide sequence of the cDNA insert of clone CO390\_1 deposited with the ATCC under accession number 98232;
  - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
  - (iii) amplifying human DNA sequences; and
  - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:60, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:60 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:60, but excluding the poly(A) tail at the 3' end of SEQ ID NO:60. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:60 from nucleotide 87 to nucleotide 1871, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:60 from nucleotide 87 to nucleotide 1871, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:60 from

nucleotide 87 to nucleotide 1871. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:60 from nucleotide 628 to nucleotide 1882, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:60 from nucleotide 628 to  
5 nucleotide 1882, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:60 from nucleotide 628 to nucleotide 1882.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:61;
- 10 (b) the amino acid sequence of SEQ ID NO:61 from amino acid 182 to amino acid 248;
- (c) a fragment of the amino acid sequence of SEQ ID NO:61, the fragment comprising eight contiguous amino acids of SEQ ID NO:61; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CO390\_1  
15 deposited with the ATCC under accession number 98232;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:61 or the amino acid sequence of SEQ ID NO:61 from amino acid 182 to amino acid 248. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:61  
20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:61, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:61 having biological activity, the fragment comprising the amino acid sequence from amino acid 292 to amino acid 301 of SEQ ID NO:61.

25 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:62;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:62  
from nucleotide 68 to nucleotide 430;
- 30 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:62 from nucleotide 128 to nucleotide 430;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AJ20\_2 deposited with the ATCC under accession number 98261;

- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AJ20\_2 deposited with the ATCC under accession number 98261;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AJ20\_2 deposited with the ATCC under accession number 98261;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AJ20\_2 deposited with the ATCC under accession number 98261;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:63;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:63 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:63;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:62.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:62 from nucleotide 68 to nucleotide 430; the nucleotide sequence of SEQ ID NO:62 from nucleotide 128 to nucleotide 430; the nucleotide sequence of the full-length protein coding sequence of clone AJ20\_2 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature protein coding sequence of clone AJ20\_2 deposited with the ATCC under accession number 98261. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AJ20\_2 deposited with the ATCC under accession number 98261. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:63 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:63, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:63 having biological activity, the fragment comprising the amino acid sequence from amino acid 55 to amino acid 64 of SEQ ID NO:63.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:62 and SEQ ID NO:64.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5                   (a)     a process comprising the steps of:
- (i)     preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa)   SEQ ID NO:62;
- 10                       (ab)   SEQ ID NO:64, but excluding the poly(A) tail at the 3' end of SEQ ID NO:64; and
- (ac)   the nucleotide sequence of the cDNA insert of clone AJ20\_2 deposited with the ATCC under accession number 98261;
- (ii)    hybridizing said probe(s) to human genomic DNA in conditions
- 15                   at least as stringent as 4X SSC at 50 degrees C; and
- (iii)   isolating the DNA polynucleotides detected with the probe(s);
- and
- (b)     a process comprising the steps of:
- (i)     preparing one or more polynucleotide primers that hybridize in
- 20                   6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba)   SEQ ID NO:62;
- (bb)   SEQ ID NO:64, but excluding the poly(A) tail at the 3' end of SEQ ID NO:64; and
- 25                        (bc)   the nucleotide sequence of the cDNA insert of clone AJ20\_2 deposited with the ATCC under accession number 98261;
- (ii)    hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii)   amplifying human DNA sequences; and
- 30                   (iv)   isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:62 and SEQ ID NO:64, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:62 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:64, but excluding the poly(A) tail at the 3' end of SEQ ID NO:64. Also preferably the polynucleotide isolated according to the

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above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:62, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:62 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:62. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide  
5 sequence corresponding to the cDNA sequence of SEQ ID NO:62 from nucleotide 68 to nucleotide 430, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:62 from nucleotide 68 to nucleotide 430, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:62 from nucleotide 68 to nucleotide 430. Also preferably the polynucleotide isolated according to the above process  
10 comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:62 from nucleotide 128 to nucleotide 430; and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:62 from nucleotide 128 to nucleotide 430, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:62 from nucleotide 128 to nucleotide 430.

15 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:63;
- (b) a fragment of the amino acid sequence of SEQ ID NO:63, the fragment comprising eight contiguous amino acids of SEQ ID NO:63; and
- 20 (c) the amino acid sequence encoded by the cDNA insert of clone AJ20\_2 deposited with the ATCC under accession number 98261;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:63. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ  
25 ID NO:63 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:63, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:63 having biological activity, the fragment comprising the amino acid sequence from amino acid 55 to amino acid 64 of SEQ ID NO:63.

In one embodiment, the present invention provides a composition comprising an isolated  
30 polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:66;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:66 from nucleotide 289 to nucleotide 780;

- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AR440\_1 deposited with the ATCC under accession number 98261;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AR440\_1 deposited with the ATCC under accession number 98261;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AR440\_1 deposited with the ATCC under accession number 98261;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AR440\_1 deposited with the ATCC under accession number 98261;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:67;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:67 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:67;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:66.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:66 from nucleotide 289 to nucleotide 780; the nucleotide sequence of the full-length protein coding sequence of clone AR440\_1 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature protein coding sequence of clone AR440\_1 deposited with the ATCC under accession number 98261. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AR440\_1 deposited with the ATCC under accession number 98261. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:67 from amino acid 1 to amino acid 160. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:67 having biological activity, the fragment

preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:67, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:67 having biological activity, the fragment comprising the amino acid sequence from amino acid 77 to amino acid 86 of SEQ ID NO:67.

- 5           Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:66 and SEQ ID NO:65.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a)     a process comprising the steps of:
- 10           (i)     preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa)   SEQ ID NO:65;
- (ab)   SEQ ID NO:66, but excluding the poly(A) tail at the 3'
- 15           end of SEQ ID NO:66; and
- (ac)   the nucleotide sequence of the cDNA insert of clone AR440\_1 deposited with the ATCC under accession number 98261;
- (ii)   hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 20           (iii)   isolating the DNA polynucleotides detected with the probe(s);
- and
- (b)     a process comprising the steps of:
- (i)     preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
- 25           consisting of:
- (ba)   SEQ ID NO:65;
- (bb)   SEQ ID NO:66, but excluding the poly(A) tail at the 3'
- end of SEQ ID NO:66; and
- (bc)   the nucleotide sequence of the cDNA insert of clone
- 30           AR440\_1 deposited with the ATCC under accession number 98261;
- (ii)   hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii)   amplifying human DNA sequences; and
- (iv)   isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:65 and SEQ ID NO:66, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:65 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:66, but excluding the poly(A) tail at the 3' end of SEQ ID NO:66. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:66, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:66 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:66, but excluding the poly(A) tail at the 3' end of SEQ ID NO:66. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:66 from nucleotide 289 to nucleotide 780, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:66 from nucleotide 289 to nucleotide 780, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:66 from nucleotide 289 to nucleotide 780.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:67;
- (b) the amino acid sequence of SEQ ID NO:67 from amino acid 1 to amino acid 160;
- (c) a fragment of the amino acid sequence of SEQ ID NO:67, the fragment comprising eight contiguous amino acids of SEQ ID NO:67; and
- (d) the amino acid sequence encoded by the cDNA insert of clone AR440\_1 deposited with the ATCC under accession number 98261;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:67 or the amino acid sequence of SEQ ID NO:67 from amino acid 1 to amino acid 160. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:67 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:67, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:67 having biological activity, the fragment comprising the amino acid sequence from amino acid 77 to amino acid 86 of SEQ ID NO:67.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:68;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:68 from nucleotide 76 to nucleotide 1050;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:68 from nucleotide 331 to nucleotide 567;
- 5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AS164\_1 deposited with the ATCC under accession number 98261;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AS164\_1 deposited with the ATCC under accession number 98261;
- 10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AS164\_1 deposited with the ATCC under accession number 98261;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AS164\_1 deposited with the ATCC under accession number 98261;
- 15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:69;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:69 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:69;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 25 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:68.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:68 from nucleotide 76 to nucleotide 1050; the nucleotide sequence of SEQ ID NO:68 from nucleotide 331 to nucleotide 567; the nucleotide sequence of the full-length protein coding sequence of clone AS164\_1 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature protein coding sequence of clone AS164\_1 deposited with the ATCC under accession number 98261. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AS164\_1

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deposited with the ATCC under accession number 98261. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:69 from amino acid 87 to amino acid 164. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a  
5 fragment of the amino acid sequence of SEQ ID NO:69 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:69, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:69 having biological activity, the fragment comprising the amino acid sequence from amino acid 157 to amino acid 166 of SEQ ID NO:69.

10 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:68.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:  
15 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:68, but excluding the poly(A) tail at the 3' end of SEQ ID NO:68; and  
20 (ab) the nucleotide sequence of the cDNA insert of clone AS164\_1 deposited with the ATCC under accession number 98261;  
(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and  
(iii) isolating the DNA polynucleotides detected with the probe(s);

25 and

(b) a process comprising the steps of:  
(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (ba) SEQ ID NO:68, but excluding the poly(A) tail at the 3' end of SEQ ID NO:68; and

(bb) the nucleotide sequence of the cDNA insert of clone AS164\_1 deposited with the ATCC under accession number 98261;

(ii) hybridizing said primer(s) to human genomic DNA in conditions  
35 at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:68, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:68 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:68, but excluding the poly(A) tail at the 3' end of SEQ ID NO:68. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:68 from nucleotide 76 to nucleotide 1050, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:68 from nucleotide 76 to nucleotide 1050, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:68 from nucleotide 76 to nucleotide 1050. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:68 from nucleotide 331 to nucleotide 567, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:68 from nucleotide 331 to nucleotide 567, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:68 from nucleotide 331 to nucleotide 567.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:69;
- (b) the amino acid sequence of SEQ ID NO:69 from amino acid 87 to amino acid 164;
- (c) a fragment of the amino acid sequence of SEQ ID NO:69, the fragment comprising eight contiguous amino acids of SEQ ID NO:69; and
- (d) the amino acid sequence encoded by the cDNA insert of clone AS164\_1 deposited with the ATCC under accession number 98261;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:69 or the amino acid sequence of SEQ ID NO:69 from amino acid 87 to amino acid 164. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:69 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:69, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:69 having biological activity, the fragment comprising the amino acid sequence from amino acid 157 to amino acid 166 of SEQ ID NO:69.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:70;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:70  
5 from nucleotide 242 to nucleotide 1060;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:70  
from nucleotide 596 to nucleotide 1060;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:70  
from nucleotide 10 to nucleotide 373;
- 10 (e) a polynucleotide comprising the nucleotide sequence of the full-length  
protein coding sequence of clone AX8\_1 deposited with the ATCC under accession  
number 98261;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA  
insert of clone AX8\_1 deposited with the ATCC under accession number 98261;
- 15 (g) a polynucleotide comprising the nucleotide sequence of a mature protein  
coding sequence of clone AX8\_1 deposited with the ATCC under accession number  
98261;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert  
of clone AX8\_1 deposited with the ATCC under accession number 98261;
- 20 (i) a polynucleotide encoding a protein comprising the amino acid sequence  
of SEQ ID NO:71;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino  
acid sequence of SEQ ID NO:71 having biological activity, the fragment comprising eight  
contiguous amino acids of SEQ ID NO:71;
- 25 (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h)  
above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i)  
or (j) above ;
- (m) a polynucleotide that hybridizes under stringent conditions to any one of  
30 the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of  
the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the  
length of SEQ ID NO:70.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:70  
35 from nucleotide 242 to nucleotide 1060; the nucleotide sequence of SEQ ID NO:70 from



nucleotide 596 to nucleotide 1060; the nucleotide sequence of SEQ ID NO:70 from nucleotide 10 to nucleotide 373; the nucleotide sequence of the full-length protein coding sequence of clone AX8\_1 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature protein coding sequence of clone AX8\_1 deposited with the ATCC under accession  
5 number 98261. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AX8\_1 deposited with the ATCC under accession number 98261. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:71 from amino acid 1 to amino acid 44. In further preferred embodiments, the present invention provides  
10 a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:71 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:71, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:71 having biological activity, the fragment comprising the amino acid sequence from amino acid 131 to  
15 amino acid 140 of SEQ ID NO:71.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:70.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 20 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:70, but excluding the poly(A) tail at the 3'  
25 end of SEQ ID NO:70; and
- (ab) the nucleotide sequence of the cDNA insert of clone AX8\_1 deposited with the ATCC under accession number 98261;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 30 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group  
35 consisting of:

(ba) SEQ ID NO:70, but excluding the poly(A) tail at the 3' end of SEQ ID NO:70; and

(bb) the nucleotide sequence of the cDNA insert of clone AX8\_1 deposited with the ATCC under accession number 98261;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide  
10 sequence corresponding to the cDNA sequence of SEQ ID NO:70, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:70 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:70, but excluding the poly(A) tail at the 3' end of SEQ ID NO:70. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:70 from nucleotide  
15 242 to nucleotide 1060, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:70 from nucleotide 242 to nucleotide 1060, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:70 from nucleotide 242 to nucleotide 1060. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
20 NO:70 from nucleotide 596 to nucleotide 1060, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:70 from nucleotide 596 to nucleotide 1060, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:70 from nucleotide 596 to nucleotide 1060. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA  
25 sequence of SEQ ID NO:70 from nucleotide 10 to nucleotide 373, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:70 from nucleotide 10 to nucleotide 373, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:70 from nucleotide 10 to nucleotide 373.

In other embodiments, the present invention provides a composition comprising a protein,  
30 wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:71;

(b) the amino acid sequence of SEQ ID NO:71 from amino acid 1 to amino acid 44;

(c) a fragment of the amino acid sequence of SEQ ID NO:71, the fragment  
35 comprising eight contiguous amino acids of SEQ ID NO:71; and

(d) the amino acid sequence encoded by the cDNA insert of clone AX8\_1 deposited with the ATCC under accession number 98261;  
the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:71 or the amino acid sequence of SEQ ID NO:71 from amino acid 1 to amino acid 44. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:71 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:71, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:71 having biological activity, the fragment comprising the amino acid sequence from amino acid 131 to amino acid 140 of SEQ ID NO:71.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:72;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:72 from nucleotide 773 to nucleotide 928;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:72 from nucleotide 815 to nucleotide 928;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BD176\_3 deposited with the ATCC under accession number 98261;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BD176\_3 deposited with the ATCC under accession number 98261;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BD176\_3 deposited with the ATCC under accession number 98261;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BD176\_3 deposited with the ATCC under accession number 98261;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:73;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:73 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:73;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

5 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:72.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:72 from nucleotide 773 to nucleotide 928; the nucleotide sequence of SEQ ID NO:72 from nucleotide  
10 815 to nucleotide 928; the nucleotide sequence of the full-length protein coding sequence of clone BD176\_3 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature protein coding sequence of clone BD176\_3 deposited with the ATCC under accession number 98261. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BD176\_3 deposited with the ATCC under  
15 accession number 98261. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:73 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:73, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:73 having  
20 biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:73.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:72 and SEQ ID NO:74.

Further embodiments of the invention provide isolated polynucleotides produced  
25 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (aa) SEQ ID NO:72;

(ab) SEQ ID NO:74, but excluding the poly(A) tail at the 3' end of SEQ ID NO:74; and

(ac) the nucleotide sequence of the cDNA insert of clone BD176\_3 deposited with the ATCC under accession number 98261;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

5 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:72;

10 (bb) SEQ ID NO:74, but excluding the poly(A) tail at the 3' end of SEQ ID NO:74; and

(bc) the nucleotide sequence of the cDNA insert of clone BD176\_3 deposited with the ATCC under accession number 98261;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

15 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:72 and SEQ ID NO:74, and  
20 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:72 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:74, but excluding the poly(A) tail at the 3' end of SEQ ID NO:74. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:72, and extending contiguously from a nucleotide sequence corresponding to the 5' end of  
25 SEQ ID NO:72 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:72. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:72 from nucleotide 773 to nucleotide 928, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:72 from nucleotide 773 to nucleotide 928, to a nucleotide  
30 sequence corresponding to the 3' end of said sequence of SEQ ID NO:72 from nucleotide 773 to nucleotide 928. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:72 from nucleotide 815 to nucleotide 928, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:72 from nucleotide 815 to nucleotide

928, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:72 from nucleotide 815 to nucleotide 928.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 5           (a)     the amino acid sequence of SEQ ID NO:73;
- (b)     a fragment of the amino acid sequence of SEQ ID NO:73, the fragment comprising eight contiguous amino acids of SEQ ID NO:73; and
- (c)     the amino acid sequence encoded by the cDNA insert of clone BD176\_3 deposited with the ATCC under accession number 98261;
- 10   the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:73. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:73 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:73, or a protein comprising
- 15   a fragment of the amino acid sequence of SEQ ID NO:73 having biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:73.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75;
- 20          (b)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75 from nucleotide 174 to nucleotide 440;
- (c)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75 from nucleotide 1 to nucleotide 313;
- (d)     a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BD339\_1 deposited with the ATCC under accession
- 25          number 98261;
- (e)     a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BD339\_1 deposited with the ATCC under accession number 98261;
- (f)     a polynucleotide comprising the nucleotide sequence of a mature protein
- 30          coding sequence of clone BD339\_1 deposited with the ATCC under accession number 98261;
- (g)     a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BD339\_1 deposited with the ATCC under accession number 98261;
- (h)     a polynucleotide encoding a protein comprising the amino acid sequence
- 35          of SEQ ID NO:76;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:76;

5 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

10 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:75.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:75 from nucleotide 174 to nucleotide 440; the nucleotide sequence of SEQ ID NO:75 from  
15 nucleotide 1 to nucleotide 313; the nucleotide sequence of the full-length protein coding sequence of clone BD339\_1 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature protein coding sequence of clone BD339\_1 deposited with the ATCC under accession number 98261. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BD339\_1 deposited with the  
20 ATCC under accession number 98261. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:76 from amino acid 1 to amino acid 46. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment preferably comprising eight  
25 (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:76, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising the amino acid sequence from amino acid 39 to amino acid 48 of SEQ ID NO:76.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID  
30 NO:75.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and

(ab) the nucleotide sequence of the cDNA insert of clone BD339\_1 deposited with the ATCC under accession number 98261;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and

(bb) the nucleotide sequence of the cDNA insert of clone BD339\_1 deposited with the ATCC under accession number 98261;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:75 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75 from nucleotide 174 to nucleotide 440, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:75 from nucleotide 174 to nucleotide 440, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:75 from nucleotide 174 to nucleotide 440. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75 from nucleotide 1 to nucleotide 313, and extending contiguously from a nucleotide



sequence corresponding to the 5' end of said sequence of SEQ ID NO:75 from nucleotide 1 to nucleotide 313, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:75 from nucleotide 1 to nucleotide 313.

In other embodiments, the present invention provides a composition comprising a protein,  
5 wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:76;
- (b) the amino acid sequence of SEQ ID NO:76 from amino acid 1 to amino acid 46;
- (c) a fragment of the amino acid sequence of SEQ ID NO:76, the fragment  
10 comprising eight contiguous amino acids of SEQ ID NO:76; and
- (d) the amino acid sequence encoded by the cDNA insert of clone BD339\_1 deposited with the ATCC under accession number 98261;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:76 or the amino acid sequence of SEQ ID  
15 NO:76 from amino acid 1 to amino acid 46. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:76, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment  
20 comprising the amino acid sequence from amino acid 39 to amino acid 48 of SEQ ID NO:76.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77  
25 from nucleotide 509 to nucleotide 619;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77 from nucleotide 1 to nucleotide 580;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BD427\_1 deposited with the ATCC under accession  
30 number 98261;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BD427\_1 deposited with the ATCC under accession number 98261;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BD427\_1 deposited with the ATCC under accession number  
35 98261;

- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BD427\_1 deposited with the ATCC under accession number 98261;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:78;
- 5 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:78;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- 10 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:77.
- 15

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:77 from nucleotide 509 to nucleotide 619; the nucleotide sequence of SEQ ID NO:77 from nucleotide 1 to nucleotide 580; the nucleotide sequence of the full-length protein coding sequence of clone BD427\_1 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature protein coding sequence of clone BD427\_1 deposited with the ATCC under accession number 98261. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BD427\_1 deposited with the ATCC under accession number 98261. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:78 from amino acid 1 to amino acid 24. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:78, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 13 to amino acid 22 of SEQ ID NO:78.

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Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:77.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and

(ab) the nucleotide sequence of the cDNA insert of clone BD427\_1 deposited with the ATCC under accession number 98261;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and

(bb) the nucleotide sequence of the cDNA insert of clone BD427\_1 deposited with the ATCC under accession number 98261;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:77 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77 from nucleotide 509 to nucleotide 619, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:77 from nucleotide 509 to nucleotide 619, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:77 from

nucleotide 509 to nucleotide 619. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77 from nucleotide 1 to nucleotide 580, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:77 from nucleotide 1 to nucleotide 580, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:77 from nucleotide 1 to nucleotide 580.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:78;
- 10 (b) the amino acid sequence of SEQ ID NO:78 from amino acid 1 to amino acid 24;
- (c) a fragment of the amino acid sequence of SEQ ID NO:78, the fragment comprising eight contiguous amino acids of SEQ ID NO:78; and
- (d) the amino acid sequence encoded by the cDNA insert of clone BD427\_1
- 15 deposited with the ATCC under accession number 98261;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:78 or the amino acid sequence of SEQ ID NO:78 from amino acid 1 to amino acid 24. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:78, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 13 to amino acid 22 of SEQ ID NO:78.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79 from nucleotide 300 to nucleotide 360;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BL229\_22 deposited with the ATCC under accession number 98261;
- 30 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BL229\_22 deposited with the ATCC under accession number 98261;

- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BL229\_22 deposited with the ATCC under accession number 98261;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BL229\_22 deposited with the ATCC under accession number 98261;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:80;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:80;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:79.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:79 from nucleotide 300 to nucleotide 360; the nucleotide sequence of the full-length protein coding sequence of clone BL229\_22 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature protein coding sequence of clone BL229\_22 deposited with the ATCC under accession number 98261. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BL229\_22 deposited with the ATCC under accession number 98261. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:80, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising the amino acid sequence from amino acid 5 to amino acid 14 of SEQ ID NO:80.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:79 and SEQ ID NO:81.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X

5 SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:79;

(ab) SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81; and

10 (ac) the nucleotide sequence of the cDNA insert of clone BL229\_22 deposited with the ATCC under accession number 98261;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

15 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

20 (ba) SEQ ID NO:79;

(bb) SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81; and

(bc) the nucleotide sequence of the cDNA insert of clone BL229\_22 deposited with the ATCC under accession number 98261;

25 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide  
30 sequence corresponding to the cDNA sequences of SEQ ID NO:79 and SEQ ID NO:81, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:79 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
35 NO:79, and extending contiguously from a nucleotide sequence corresponding to the 5' end of

SEQ ID NO:79 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:79. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79 from nucleotide 300 to nucleotide 360, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:79 from nucleotide 300 to nucleotide 360, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:79 from nucleotide 300 to nucleotide 360.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:80;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:80, the fragment comprising eight contiguous amino acids of SEQ ID NO:80; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone BL229\_22 deposited with the ATCC under accession number 98261;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:80. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:80, or a protein comprising
- 20 a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising the amino acid sequence from amino acid 5 to amino acid 14 of SEQ ID NO:80.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:82;
- 25 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:82 from nucleotide 604 to nucleotide 771;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:82 from nucleotide 1 to nucleotide 684;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length
- 30 protein coding sequence of clone BV123\_16 deposited with the ATCC under accession number 98261;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BV123\_16 deposited with the ATCC under accession number 98261;

- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BV123\_16 deposited with the ATCC under accession number 98261;
- 5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BV123\_16 deposited with the ATCC under accession number 98261;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:83;
- 10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:83 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:83;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 15 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:82.
- 20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:82 from nucleotide 604 to nucleotide 771; the nucleotide sequence of SEQ ID NO:82 from nucleotide 1 to nucleotide 684; the nucleotide sequence of the full-length protein coding sequence of clone BV123\_16 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature protein coding sequence of clone BV123\_16 deposited with the ATCC under
- 25 accession number 98261. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BV123\_16 deposited with the ATCC under accession number 98261. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:83 from amino acid 1 to amino acid 27. In further preferred embodiments, the present
- 30 invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:83 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:83, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:83 having biological activity, the fragment comprising the amino acid sequence from amino
- 35 acid 23 to amino acid 32 of SEQ ID NO:83.



Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:82.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5                   (a)     a process comprising the steps of:
- (i)     preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa)   SEQ ID NO:82, but excluding the poly(A) tail at the 3'
- 10                       end of SEQ ID NO:82; and
- (ab)   the nucleotide sequence of the cDNA insert of clone BV123\_16 deposited with the ATCC under accession number 98261;
- (ii)    hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 15                       (iii)   isolating the DNA polynucleotides detected with the probe(s);
- and
- (b)     a process comprising the steps of:
- (i)     preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
- 20                       consisting of:
- (ba)   SEQ ID NO:82, but excluding the poly(A) tail at the 3' end of SEQ ID NO:82; and
- (bb)   the nucleotide sequence of the cDNA insert of clone BV123\_16 deposited with the ATCC under accession number 98261;
- 25                       (ii)    hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii)   amplifying human DNA sequences; and
- (iv)   isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide

30   sequence corresponding to the cDNA sequence of SEQ ID NO:82, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:82 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:82, but excluding the poly(A) tail at the 3' end of SEQ ID NO:82. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:82 from nucleotide

35   604 to nucleotide 771, and extending contiguously from a nucleotide sequence corresponding to

the 5' end of said sequence f SEQ ID NO:82 from nucleotide 604 to nucleotide 771, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:82 from nucleotide 604 to nucleotide 771. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
5 NO:82 from nucleotide 1 to nucleotide 684, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:82 from nucleotide 1 to nucleotide 684, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:82 from nucleotide 1 to nucleotide 684.

In other embodiments, the present invention provides a composition comprising a protein,  
10 wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:83;
- (b) the amino acid sequence of SEQ ID NO:83 from amino acid 1 to amino acid 27;
- (c) a fragment of the amino acid sequence of SEQ ID NO:83, the fragment  
15 comprising eight contiguous amino acids of SEQ ID NO:83; and
- (d) the amino acid sequence encoded by the cDNA insert of clone BV123\_16 deposited with the ATCC under accession number 98261;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:83 or the amino acid sequence of SEQ ID  
20 NO:83 from amino acid 1 to amino acid 27. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:83 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:83, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:83 having biological activity, the fragment  
25 comprising the amino acid sequence from amino acid 23 to amino acid 32 of SEQ ID NO:83.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:84;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:84  
30 from nucleotide 43 to nucleotide 297;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:84 from nucleotide 94 to nucleotide 297;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:84 from nucleotide 1 to nucleotide 379;

- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CH377\_1 deposited with the ATCC under accession number 98261;
- 5 (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CH377\_1 deposited with the ATCC under accession number 98261;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CH377\_1 deposited with the ATCC under accession number 98261;
- 10 (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CH377\_1 deposited with the ATCC under accession number 98261;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:85;
- 15 (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:85 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:85;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- 20 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:84.
- 25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:84 from nucleotide 43 to nucleotide 297; the nucleotide sequence of SEQ ID NO:84 from nucleotide 94 to nucleotide 297; the nucleotide sequence of SEQ ID NO:84 from nucleotide 1 to nucleotide 379; the nucleotide sequence of the full-length protein coding sequence of clone CH377\_1 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature
- 30 protein coding sequence of clone CH377\_1 deposited with the ATCC under accession number 98261. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CH377\_1 deposited with the ATCC under accession number 98261. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID
- 35 NO:85 having biological activity, the fragment preferably comprising eight (more preferably

twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:85, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:85 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID NO:85.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:84.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - 10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:84, but excluding the poly(A) tail at the 3' end of SEQ ID NO:84; and
    - 15 (ab) the nucleotide sequence of the cDNA insert of clone CH377\_1 deposited with the ATCC under accession number 98261;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
  - 20 and
  - (b) a process comprising the steps of:
    - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
      - 25 (ba) SEQ ID NO:84, but excluding the poly(A) tail at the 3' end of SEQ ID NO:84; and
      - (bb) the nucleotide sequence of the cDNA insert of clone CH377\_1 deposited with the ATCC under accession number 98261;
      - (ii) hybridizing said primer(s) to human genomic DNA in conditions
      - 30 at least as stringent as 4X SSC at 50 degrees C;
      - (iii) amplifying human DNA sequences; and
      - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:84, and extending contiguously

35 from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:84 to a nucleotide sequence

corresponding to the 3' end of SEQ ID NO:84, but excluding the poly(A) tail at the 3' end of SEQ ID NO:84. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:84 from nucleotide 43 to nucleotide 297, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:84 from nucleotide 43 to nucleotide 297, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:84 from nucleotide 43 to nucleotide 297. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:84 from nucleotide 94 to nucleotide 297, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:84 from nucleotide 94 to nucleotide 297, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:84 from nucleotide 94 to nucleotide 297. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:84 from nucleotide 1 to nucleotide 379, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:84 from nucleotide 1 to nucleotide 379, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:84 from nucleotide 1 to nucleotide 379.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:85;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:85, the fragment comprising eight contiguous amino acids of SEQ ID NO:85; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone CH377\_1 deposited with the ATCC under accession number 98261;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:85. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:85 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:85, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:85 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID NO:85.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87 from nucleotide 390 to nucleotide 563;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BD441\_1 deposited with the ATCC under accession number 98264;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BD441\_1 deposited with the ATCC under accession number 98264;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BD441\_1 deposited with the ATCC under accession number 98264;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BD441\_1 deposited with the ATCC under accession number 98264;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:88;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:88;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:87.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:87 from nucleotide 390 to nucleotide 563; the nucleotide sequence of the full-length protein coding sequence of clone BD441\_1 deposited with the ATCC under accession number 98264; or the nucleotide sequence of a mature protein coding sequence of clone BD441\_1 deposited with the ATCC under accession number 98264. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BD441\_1 deposited with the ATCC under accession number 98264. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:88, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising the amino acid sequence from amino acid 24 to amino acid 33 of SEQ ID NO:88.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:87, SEQ ID NO:86, and SEQ ID NO:89.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - 10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:86;
    - (ab) SEQ ID NO:87;
    - 15 (ac) SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89; and
    - (ad) the nucleotide sequence of the cDNA insert of clone BD441\_1 deposited with the ATCC under accession number 98264;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions
    - 20 at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in
  - 25 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:86;
    - (bb) SEQ ID NO:87;
    - (bc) SEQ ID NO:89, but excluding the poly(A) tail at the 3'
    - 30 end of SEQ ID NO:89; and
    - (bd) the nucleotide sequence of the cDNA insert of clone BD441\_1 deposited with the ATCC under accession number 98264;
    - (ii) hybridizing said primer(s) to human genomic DNA in conditions
    - at least as stringent as 4X SSC at 50 degrees C;
    - 35 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:86, SEQ ID NO:87, and SEQ ID NO:89, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:86 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:87 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:87. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87 from nucleotide 390 to nucleotide 563, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:87 from nucleotide 390 to nucleotide 563, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:87 from nucleotide 390 to nucleotide 563.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:88;
- (b) a fragment of the amino acid sequence of SEQ ID NO:88, the fragment comprising eight contiguous amino acids of SEQ ID NO:88; and
- (c) the amino acid sequence encoded by the cDNA insert of clone BD441\_1 deposited with the ATCC under accession number 98264;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:88. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:88, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising the amino acid sequence from amino acid 24 to amino acid 33 of SEQ ID NO:88.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:90;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:90 from nucleotide 583 to nucleotide 756;



- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BD441\_2 deposited with the ATCC under accession number 98264;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BD441\_2 deposited with the ATCC under accession number 98264;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BD441\_2 deposited with the ATCC under accession number 98264;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BD441\_2 deposited with the ATCC under accession number 98264;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:91;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:91 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:91;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:90.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:90 from nucleotide 583 to nucleotide 756; the nucleotide sequence of the full-length protein coding sequence of clone BD441\_2 deposited with the ATCC under accession number 98264; or the nucleotide sequence of a mature protein coding sequence of clone BD441\_2 deposited with the ATCC under accession number 98264. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BD441\_2 deposited with the ATCC under accession number 98264. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:91 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:91, or a polynucleotide encoding a protein comprising a fragment of the amino acid

sequence of SEQ ID NO:91 having biological activity, the fragment comprising the amino acid sequence from amino acid 24 to amino acid 33 of SEQ ID NO:91.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:90 and SEQ ID NO:92.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X  
10 SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:90;

(ab) SEQ ID NO:92, but excluding the poly(A) tail at the 3'  
end of SEQ ID NO:92; and

(ac) the nucleotide sequence of the cDNA insert of clone  
15 BD441\_2 deposited with the ATCC under accession number 98264;

(ii) hybridizing said probe(s) to human genomic DNA in conditions  
at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in  
6X SSC at 65 degrees C to a nucleotide sequence selected from the group  
consisting of:

(ba) SEQ ID NO:90;

25 (bb) SEQ ID NO:92, but excluding the poly(A) tail at the 3'  
end of SEQ ID NO:92; and

(bc) the nucleotide sequence of the cDNA insert of clone  
BD441\_2 deposited with the ATCC under accession number 98264;

(ii) hybridizing said primer(s) to human genomic DNA in conditions  
30 at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide  
sequence corresponding to the cDNA sequences of SEQ ID NO:90 and SEQ ID NO:92, and  
35 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:90

to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:92, but excluding the poly(A) tail at the 3' end of SEQ ID NO:92. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:90, and extending contiguously from a nucleotide sequence corresponding to the 5' end of  
5 SEQ ID NO:90 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:90. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:90 from nucleotide 583 to nucleotide 756, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:90 from nucleotide 583 to nucleotide 756, to a nucleotide  
10 sequence corresponding to the 3' end of said sequence of SEQ ID NO:90 from nucleotide 583 to nucleotide 756.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:91;
- 15 (b) a fragment of the amino acid sequence of SEQ ID NO:91, the fragment comprising eight contiguous amino acids of SEQ ID NO:91; and
- (c) the amino acid sequence encoded by the cDNA insert of clone BD441\_2 deposited with the ATCC under accession number 98264;

the protein being substantially free from other mammalian proteins. Preferably such protein  
20 comprises the amino acid sequence of SEQ ID NO:91. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:91 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:91, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:91 having biological activity, the fragment  
25 comprising the amino acid sequence from amino acid 24 to amino acid 33 of SEQ ID NO:91.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93  
30 from nucleotide 426 to nucleotide 581;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93 from nucleotide 495 to nucleotide 581;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93 from nucleotide 354 to nucleotide 503;

- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BG102\_3 deposited with the ATCC under accession number 98264;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BG102\_3 deposited with the ATCC under accession number 98264;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BG102\_3 deposited with the ATCC under accession number 98264;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BG102\_3 deposited with the ATCC under accession number 98264;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:94;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:94;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:93.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:93 from nucleotide 426 to nucleotide 581; the nucleotide sequence of SEQ ID NO:93 from nucleotide 495 to nucleotide 581; the nucleotide sequence of SEQ ID NO:93 from nucleotide 354 to nucleotide 503; the nucleotide sequence of the full-length protein coding sequence of clone BG102\_3 deposited with the ATCC under accession number 98264; or the nucleotide sequence of a mature protein coding sequence of clone BG102\_3 deposited with the ATCC under accession number 98264. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BG102\_3 deposited with the ATCC under accession number 98264. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:94 from amino acid 1 to amino acid 26. In further preferred embodiments, the present invention provides

a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:94, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having  
5 biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:94.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:93.

Further embodiments of the invention provide isolated polynucleotides produced  
10 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

15 (aa) SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93; and

(ab) the nucleotide sequence of the cDNA insert of clone BG102\_3 deposited with the ATCC under accession number 98264;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93; and

30 (bb) the nucleotide sequence of the cDNA insert of clone BG102\_3 deposited with the ATCC under accession number 98264;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:93 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93 from nucleotide 426 to nucleotide 581, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:93 from nucleotide 426 to nucleotide 581, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:93 from nucleotide 426 to nucleotide 581. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93 from nucleotide 495 to nucleotide 581, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:93 from nucleotide 495 to nucleotide 581, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:93 from nucleotide 495 to nucleotide 581. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93 from nucleotide 354 to nucleotide 503, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:93 from nucleotide 354 to nucleotide 503, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:93 from nucleotide 354 to nucleotide 503.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:94;
  - (b) the amino acid sequence of SEQ ID NO:94 from amino acid 1 to amino acid 26;
  - (c) a fragment of the amino acid sequence of SEQ ID NO:94, the fragment comprising eight contiguous amino acids of SEQ ID NO:94; and
  - (d) the amino acid sequence encoded by the cDNA insert of clone BG102\_3 deposited with the ATCC under accession number 98264;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:94 or the amino acid sequence of SEQ ID NO:94 from amino acid 1 to amino acid 26. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:94, or a protein comprising a

fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:94.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5                   (a)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95;
- (b)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95  
                  from nucleotide 112 to nucleotide 978;
- (c)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95  
                  from nucleotide 436 to nucleotide 1048;
- 10               (d)     a polynucleotide comprising the nucleotide sequence of the full-length  
                  protein coding sequence of clone BK158\_1 deposited with the ATCC under accession  
                  number 98264;
- (e)     a polynucleotide encoding the full-length protein encoded by the cDNA  
                  insert of clone BK158\_1 deposited with the ATCC under accession number 98264;
- 15               (f)     a polynucleotide comprising the nucleotide sequence of a mature protein  
                  coding sequence of clone BK158\_1 deposited with the ATCC under accession number  
                  98264;
- (g)     a polynucleotide encoding a mature protein encoded by the cDNA insert  
                  of clone BK158\_1 deposited with the ATCC under accession number 98264;
- 20               (h)     a polynucleotide encoding a protein comprising the amino acid sequence  
                  of SEQ ID NO:96;
- (i)     a polynucleotide encoding a protein comprising a fragment of the amino  
                  acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising eight  
                  contiguous amino acids of SEQ ID NO:96;
- 25               (j)     a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g)  
                  above;
- (k)     a polynucleotide which encodes a species homologue of the protein of (h)  
                  or (i) above ;
- (l)     a polynucleotide that hybridizes under stringent conditions to any one of  
30               the polynucleotides specified in (a)-(i); and
- (m)     a polynucleotide that hybridizes under stringent conditions to any one of  
                  the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the  
                  length of SEQ ID NO:95.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:95  
35   from nucleotide 112 to nucleotide 978; the nucleotide sequence of SEQ ID NO:95 from

nucleotide 436 to nucleotide 1048; the nucleotide sequence of the full-length protein coding sequence of clone BK158\_1 deposited with the ATCC under accession number 98264; or the nucleotide sequence of a mature protein coding sequence of clone BK158\_1 deposited with the ATCC under accession number 98264. In other preferred embodiments, the polynucleotide  
5 encodes the full-length or a mature protein encoded by the cDNA insert of clone BK158\_1 deposited with the ATCC under accession number 98264. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ  
10 ID NO:96, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising the amino acid sequence from amino acid 139 to amino acid 148 of SEQ ID NO:96.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:95.

15 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X  
SSC at 65 degrees C to a nucleotide sequence selected from the group consisting  
20 of:

(aa) SEQ ID NO:95, but excluding the poly(A) tail at the 3'  
end of SEQ ID NO:95; and

(ab) the nucleotide sequence of the cDNA insert of clone  
BK158\_1 deposited with the ATCC under accession number 98264;

25 (ii) hybridizing said probe(s) to human genomic DNA in conditions  
at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

30 (i) preparing one or more polynucleotide primers that hybridize in  
6X SSC at 65 degrees C to a nucleotide sequence selected from the group  
consisting of:

(ba) SEQ ID NO:95, but excluding the poly(A) tail at the 3'  
end of SEQ ID NO:95; and



(bb) the nucleotide sequence of the cDNA insert of clone BK158\_1 deposited with the ATCC under accession number 98264;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

5 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:95 to a nucleotide sequence  
10 corresponding to the 3' end of SEQ ID NO:95, but excluding the poly(A) tail at the 3' end of SEQ ID NO:95. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95 from nucleotide 112 to nucleotide 978, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:95 from nucleotide 112 to nucleotide 978, to a  
15 nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:95 from nucleotide 112 to nucleotide 978. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95 from nucleotide 436 to nucleotide 1048, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:95 from nucleotide 436 to  
20 nucleotide 1048, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:95 from nucleotide 436 to nucleotide 1048.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:96;
- 25 (b) a fragment of the amino acid sequence of SEQ ID NO:96, the fragment comprising eight contiguous amino acids of SEQ ID NO:96; and
- (c) the amino acid sequence encoded by the cDNA insert of clone BK158\_1 deposited with the ATCC under accession number 98264;

the protein being substantially free from other mammalian proteins. Preferably such protein  
30 comprises the amino acid sequence of SEQ ID NO:96. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:96, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment  
35 comprising the amino acid sequence from amino acid 139 to amino acid 148 of SEQ ID NO:96.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97  
5 from nucleotide 16 to nucleotide 492;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BP163\_1 deposited with the ATCC under accession number 98264;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA  
10 insert of clone BP163\_1 deposited with the ATCC under accession number 98264;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BP163\_1 deposited with the ATCC under accession number 98264;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert  
15 of clone BP163\_1 deposited with the ATCC under accession number 98264;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:98;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising eight  
20 contiguous amino acids of SEQ ID NO:98;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of  
25 the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:97.

30 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:97 from nucleotide 16 to nucleotide 492; the nucleotide sequence of the full-length protein coding sequence of clone BP163\_1 deposited with the ATCC under accession number 98264; or the nucleotide sequence of a mature protein coding sequence of clone BP163\_1 deposited with the ATCC under accession number 98264. In other preferred embodiments, the polynucleotide  
35 encodes the full-length or a mature protein encoded by the cDNA insert of clone BP163\_1

deposited with the ATCC under accession number 98264. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:98, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising the amino acid sequence from amino acid 74 to amino acid 83 of SEQ ID NO:98.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:97 and SEQ ID NO:99.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:97;

(ab) SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99; and

(ac) the nucleotide sequence of the cDNA insert of clone BP163\_1 deposited with the ATCC under accession number 98264;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:97;

(bb) SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99; and

(bc) the nucleotide sequence of the cDNA insert of clone BP163\_1 deposited with the ATCC under accession number 98264;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:97 and SEQ ID NO:99, and  
 5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:97 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97, and extending contiguously from a nucleotide sequence corresponding to the 5' end of  
 10 SEQ ID NO:97 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:97. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97 from nucleotide 16 to nucleotide 492, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:97 from nucleotide 16 to nucleotide 492, to a nucleotide  
 15 sequence corresponding to the 3' end of said sequence of SEQ ID NO:97 from nucleotide 16 to nucleotide 492.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:98;
- 20 (b) a fragment of the amino acid sequence of SEQ ID NO:98, the fragment comprising eight contiguous amino acids of SEQ ID NO:98; and
- (c) the amino acid sequence encoded by the cDNA insert of clone BP163\_1 deposited with the ATCC under accession number 98264;

the protein being substantially free from other mammalian proteins. Preferably such protein  
 25 comprises the amino acid sequence of SEQ ID NO:98. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:98, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment  
 30 comprising the amino acid sequence from amino acid 74 to amino acid 83 of SEQ ID NO:98.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101  
 35 from nucleotide 72 to nucleotide 569;

- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BZ16\_3 deposited with the ATCC under accession number 98264;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BZ16\_3 deposited with the ATCC under accession number 98264;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BZ16\_3 deposited with the ATCC under accession number 98264;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BZ16\_3 deposited with the ATCC under accession number 98264;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:102;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:102;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:101.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:101 from nucleotide 72 to nucleotide 569; the nucleotide sequence of the full-length protein coding sequence of clone BZ16\_3 deposited with the ATCC under accession number 98264; or the nucleotide sequence of a mature protein coding sequence of clone BZ16\_3 deposited with the ATCC under accession number 98264. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BZ16\_3 deposited with the ATCC under accession number 98264. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:102 from amino acid 1 to amino acid 124. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment

preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:102, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising the amino acid sequence from amino acid 78 to amino acid 87 of SEQ ID NO:102.

- 5           Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:101 and SEQ ID NO:100.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a)     a process comprising the steps of:
- 10           (i)     preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa)   SEQ ID NO:100;
- (ab)   SEQ ID NO:101, but excluding the poly(A) tail at the 3'
- 15           end of SEQ ID NO:101; and
- (ac)   the nucleotide sequence of the cDNA insert of clone BZ16\_3 deposited with the ATCC under accession number 98264;
- (ii)   hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 20           (iii)   isolating the DNA polynucleotides detected with the probe(s);
- and
- (b)     a process comprising the steps of:
- (i)     preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
- 25           consisting of:
- (ba)   SEQ ID NO:100;
- (bb)   SEQ ID NO:101, but excluding the poly(A) tail at the 3'
- end of SEQ ID NO:101; and
- (bc)   the nucleotide sequence of the cDNA insert of clone
- 30           BZ16\_3 deposited with the ATCC under accession number 98264;
- (ii)   hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii)   amplifying human DNA sequences; and
- (iv)   isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:100 and SEQ ID NO:101, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:100 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:101 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101 from nucleotide 72 to nucleotide 569, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:101 from nucleotide 72 to nucleotide 569, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:101 from nucleotide 72 to nucleotide 569.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:102;
  - (b) the amino acid sequence of SEQ ID NO:102 from amino acid 1 to amino acid 124;
  - (c) a fragment of the amino acid sequence of SEQ ID NO:102, the fragment comprising eight contiguous amino acids of SEQ ID NO:102; and
  - (d) the amino acid sequence encoded by the cDNA insert of clone BZ16\_3 deposited with the ATCC under accession number 98264;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:102 or the amino acid sequence of SEQ ID NO:102 from amino acid 1 to amino acid 124. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:102, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising the amino acid sequence from amino acid 78 to amino acid 87 of SEQ ID NO:102.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103 from nucleotide 405 to nucleotide 662;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103 from nucleotide 519 to nucleotide 662;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103 from nucleotide 1 to nucleotide 584;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CC182\_1 deposited with the ATCC under accession number 98264;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CC182\_1 deposited with the ATCC under accession number 98264;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CC182\_1 deposited with the ATCC under accession number 98264;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CC182\_1 deposited with the ATCC under accession number 98264;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:104;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:104;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:103.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:103 from nucleotide 405 to nucleotide 662; the nucleotide sequence of SEQ ID NO:103 from nucleotide 519 to nucleotide 662; the nucleotide sequence of SEQ ID NO:103 from nucleotide 1 to nucleotide 584; the nucleotide sequence of the full-length protein coding sequence of clone



CC182\_1 deposited with the ATCC under accession number 98264; or the nucleotide sequence of a mature protein coding sequence of clone CC182\_1 deposited with the ATCC under accession number 98264. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CC182\_1 deposited with the ATCC under  
5 accession number 98264. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:104 from amino acid 1 to amino acid 60. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment preferably comprising eight (more preferably  
10 twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:104, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:104.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID  
15 NO:103.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:  
(i) preparing one or more polynucleotide probes that hybridize in 6X  
20 SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103; and  
(ab) the nucleotide sequence of the cDNA insert of clone  
25 CC182\_1 deposited with the ATCC under accession number 98264;  
(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and  
(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:  
(i) preparing one or more polynucleotide primers that hybridize in  
30 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:103, but excluding the poly(A) tail at the 3'  
35 end of SEQ ID NO:103; and

- (bb) the nucleotide sequence of the cDNA insert of clone CC182\_1 deposited with the ATCC under accession number 98264;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:103 to a nucleotide  
10 sequence corresponding to the 3' end of SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103 from nucleotide 405 to nucleotide 662, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:103 from nucleotide 405 to nucleotide  
15 662, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:103 from nucleotide 405 to nucleotide 662. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103 from nucleotide 519 to nucleotide 662, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:103 from nucleotide 519  
20 to nucleotide 662, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:103 from nucleotide 519 to nucleotide 662. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103 from nucleotide 1 to nucleotide 584, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:103 from  
25 nucleotide 1 to nucleotide 584, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:103 from nucleotide 1 to nucleotide 584.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:104;
- 30 (b) the amino acid sequence of SEQ ID NO:104 from amino acid 1 to amino acid 60;
- (c) a fragment of the amino acid sequence of SEQ ID NO:104, the fragment comprising eight contiguous amino acids of SEQ ID NO:104; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CC182\_1  
35 deposited with the ATCC under accession number 98264;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:104 or the amino acid sequence of SEQ ID NO:104 from amino acid 1 to amino acid 60. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:104, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:104.

10 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105 from nucleotide 311 to nucleotide 409;
- 15 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105 from nucleotide 24 to nucleotide 414;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CG109\_1 deposited with the ATCC under accession number 98264;
- 20 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CG109\_1 deposited with the ATCC under accession number 98264;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CG109\_1 deposited with the ATCC under accession number 98264;
- 25 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CG109\_1 deposited with the ATCC under accession number 98264;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:106;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:106;
- 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 35

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:105.

5 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:105 from nucleotide 311 to nucleotide 409; the nucleotide sequence of SEQ ID NO:105 from nucleotide 24 to nucleotide 414; the nucleotide sequence of the full-length protein coding sequence of clone CG109\_1 deposited with the ATCC under accession number 98264; or the  
10 nucleotide sequence of a mature protein coding sequence of clone CG109\_1 deposited with the ATCC under accession number 98264. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CG109\_1 deposited with the ATCC under accession number 98264. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the  
15 amino acid sequence of SEQ ID NO:106 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:106, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising the amino acid sequence from amino acid 11 to amino acid 20 of SEQ ID NO:106.

20 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:105.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

25 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105; and

30 (ab) the nucleotide sequence of the cDNA insert of clone CG109\_1 deposited with the ATCC under accession number 98264;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

35 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105; and

(bb) the nucleotide sequence of the cDNA insert of clone CG109\_1 deposited with the ATCC under accession number 98264;

10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105, and extending contiguously  
15 from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:105 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105 from nucleotide 311 to nucleotide 409, and extending contiguously from a nucleotide sequence  
20 corresponding to the 5' end of said sequence of SEQ ID NO:105 from nucleotide 311 to nucleotide 409, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:105 from nucleotide 311 to nucleotide 409. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105 from nucleotide 24 to nucleotide 414, and extending contiguously from a nucleotide  
25 sequence corresponding to the 5' end of said sequence of SEQ ID NO:105 from nucleotide 24 to nucleotide 414, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:105 from nucleotide 24 to nucleotide 414.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

30 (a) the amino acid sequence of SEQ ID NO:106;

(b) a fragment of the amino acid sequence of SEQ ID NO:106, the fragment comprising eight contiguous amino acids of SEQ ID NO:106; and

(c) the amino acid sequence encoded by the cDNA insert of clone CG109\_1 deposited with the ATCC under accession number 98264;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:106. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment preferably comprising eight (more preferably  
5 twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:106, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising the amino acid sequence from amino acid 11 to amino acid 20 of SEQ ID NO:106.

In one embodiment, the present invention provides a composition comprising an isolated  
10 polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:108;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:108 from nucleotide 471 to nucleotide 611;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length  
15 protein coding sequence of clone CJ397\_1 deposited with the ATCC under accession number 98264;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CJ397\_1 deposited with the ATCC under accession number 98264;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein  
20 coding sequence of clone CJ397\_1 deposited with the ATCC under accession number 98264;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CJ397\_1 deposited with the ATCC under accession number 98264;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence  
25 of SEQ ID NO:109;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:109 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:109;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f)  
30 above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:108.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:108  
5 from nucleotide 471 to nucleotide 611; the nucleotide sequence of the full-length protein coding sequence of clone CJ397\_1 deposited with the ATCC under accession number 98264; or the nucleotide sequence of a mature protein coding sequence of clone CJ397\_1 deposited with the ATCC under accession number 98264. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CJ397\_1  
10 deposited with the ATCC under accession number 98264. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:109 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:109, or a polynucleotide encoding a protein comprising a fragment of the amino acid  
15 sequence of SEQ ID NO:109 having biological activity, the fragment comprising the amino acid sequence from amino acid 18 to amino acid 27 of SEQ ID NO:109.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:108, SEQ ID NO:107, and SEQ ID NO:110.

Further embodiments of the invention provide isolated polynucleotides produced  
20 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (aa) SEQ ID NO:107;  
(ab) SEQ ID NO:108;  
(ac) SEQ ID NO:110, but excluding the poly(A) tail at the 3' end of SEQ ID NO:110; and

(ad) the nucleotide sequence of the cDNA insert of clone  
30 CJ397\_1 deposited with the ATCC under accession number 98264;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

35 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:107;

(bb) SEQ ID NO:108;

(bc) SEQ ID NO:110, but excluding the poly(A) tail at the 3' end of SEQ ID NO:110; and

(bd) the nucleotide sequence of the cDNA insert of clone CJ397\_1 deposited with the ATCC under accession number 98264;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:107, SEQ ID NO:108, and SEQ ID NO:110, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:107 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:110, but excluding the poly(A) tail at the 3' end of SEQ ID NO:110. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:108, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:108 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:108. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:108 from nucleotide 471 to nucleotide 611, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:108 from nucleotide 471 to nucleotide 611, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:108 from nucleotide 471 to nucleotide 611.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:109;

(b) a fragment of the amino acid sequence of SEQ ID NO:109, the fragment comprising eight contiguous amino acids of SEQ ID NO:109; and

(c) the amino acid sequence encoded by the cDNA insert of clone CJ397\_1 deposited with the ATCC under accession number 98264;



the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:109. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:109 having biological activity, the fragment preferably comprising eight (more preferably  
5 twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:109, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:109 having biological activity, the fragment comprising the amino acid sequence from amino acid 18 to amino acid 27 of SEQ ID NO:109.

In one embodiment, the present invention provides a composition comprising an isolated  
10 polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111 from nucleotide 141 to nucleotide 1532;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111  
15 from nucleotide 204 to nucleotide 1532;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111 from nucleotide 78 to nucleotide 476;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AM795\_4 deposited with the ATCC under accession  
20 number 98271;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AM795\_4 deposited with the ATCC under accession number 98271;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AM795\_4 deposited with the ATCC under accession number  
25 98271;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AM795\_4 deposited with the ATCC under accession number 98271;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:112;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino  
30 acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:112;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

5 (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:111.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:111 from nucleotide 141 to nucleotide 1532; the nucleotide sequence of SEQ ID NO:111 from  
10 nucleotide 204 to nucleotide 1532; the nucleotide sequence of SEQ ID NO:111 from nucleotide 78 to nucleotide 476; the nucleotide sequence of the full-length protein coding sequence of clone AM795\_4 deposited with the ATCC under accession number 98271; or the nucleotide sequence of a mature protein coding sequence of clone AM795\_4 deposited with the ATCC under accession number 98271. In other preferred embodiments, the polynucleotide encodes the full-length or a  
15 mature protein encoded by the cDNA insert of clone AM795\_4 deposited with the ATCC under accession number 98271. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:112 from amino acid 1 to amino acid 112. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ  
20 ID NO:112 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:112, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising the amino acid sequence from amino acid 227 to amino acid 236 of SEQ ID NO:112.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:111.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111; and

- (ab) the nucleotide sequence of the cDNA insert of clone AM795\_4 deposited with the ATCC under accession number 98271;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
- 10 consisting of:
- (ba) SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111; and
- (bb) the nucleotide sequence of the cDNA insert of clone AM795\_4 deposited with the ATCC under accession number 98271;
- 15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide

20 sequence corresponding to the cDNA sequence of SEQ ID NO:111, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:111 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111

25 from nucleotide 141 to nucleotide 1532, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:111 from nucleotide 141 to nucleotide 1532, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:111 from nucleotide 141 to nucleotide 1532. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of

30 SEQ ID NO:111 from nucleotide 204 to nucleotide 1532, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:111 from nucleotide 204 to nucleotide 1532, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:111 from nucleotide 204 to nucleotide 1532. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence

35 corresponding to the cDNA sequence of SEQ ID NO:111 from nucleotide 78 to nucleotide 476,

and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:111 from nucleotide 78 to nucleotide 476, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:111 from nucleotide 78 to nucleotide 476.

5 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:112;
- (b) the amino acid sequence of SEQ ID NO:112 from amino acid 1 to amino acid 112;
- 10 (c) a fragment of the amino acid sequence of SEQ ID NO:112, the fragment comprising eight contiguous amino acids of SEQ ID NO:112; and
- (d) the amino acid sequence encoded by the cDNA insert of clone AM795\_4 deposited with the ATCC under accession number 98271;

the protein being substantially free from other mammalian proteins. Preferably such protein  
15 comprises the amino acid sequence of SEQ ID NO:112 or the amino acid sequence of SEQ ID NO:112 from amino acid 1 to amino acid 112. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:112, or a protein  
20 comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising the amino acid sequence from amino acid 227 to amino acid 236 of SEQ ID NO:112.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:114;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:114 from nucleotide 19 to nucleotide 262;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:114 from nucleotide 91 to nucleotide 262;
- 30 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AT340\_1 deposited with the ATCC under accession number 98271;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AT340\_1 deposited with the ATCC under accession number 98271;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AT340\_1 deposited with the ATCC under accession number 98271;

5 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AT340\_1 deposited with the ATCC under accession number 98271;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:115;

10 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:115 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:115;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

15 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:114.

20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:114 from nucleotide 19 to nucleotide 262; the nucleotide sequence of SEQ ID NO:114 from nucleotide 91 to nucleotide 262; the nucleotide sequence of the full-length protein coding sequence of clone AT340\_1 deposited with the ATCC under accession number 98271; or the nucleotide sequence of a mature protein coding sequence of clone AT340\_1 deposited with the ATCC under accession  
25 number 98271. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AT340\_1 deposited with the ATCC under accession number 98271. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:115 from amino acid 1 to amino acid 66. In further preferred embodiments, the present invention provides  
30 a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:115 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:115, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:115 having biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino  
35 acid 44 of SEQ ID NO:115.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:114 and SEQ ID NO:113.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5                   (a)     a process comprising the steps of:
- (i)     preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa)   SEQ ID NO:113;
- 10                   (ab)   SEQ ID NO:114, but excluding the poly(A) tail at the 3' end of SEQ ID NO:114; and
- (ac)   the nucleotide sequence of the cDNA insert of clone AT340\_1 deposited with the ATCC under accession number 98271;
- (ii)    hybridizing said probe(s) to human genomic DNA in conditions
- 15                   at least as stringent as 4X SSC at 50 degrees C; and
- (iii)   isolating the DNA polynucleotides detected with the probe(s);
- and
- (b)     a process comprising the steps of:
- (i)     preparing one or more polynucleotide primers that hybridize in
- 20                   6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba)   SEQ ID NO:113;
- (bb)   SEQ ID NO:114, but excluding the poly(A) tail at the 3' end of SEQ ID NO:114; and
- 25                   (bc)   the nucleotide sequence of the cDNA insert of clone AT340\_1 deposited with the ATCC under accession number 98271;
- (ii)    hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii)   amplifying human DNA sequences; and
- 30                   (iv)   isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:113 and SEQ ID NO:114, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:113 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:114, but excluding

35   the poly(A) tail at the 3' end of SEQ ID NO:114. Also preferably the polynucleotide isolated

according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:114, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:114 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:114, but excluding the poly(A) tail at the 3' end of SEQ ID NO:114. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:114 from nucleotide 19 to nucleotide 262, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:114 from nucleotide 19 to nucleotide 262, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:114 from nucleotide 19 to nucleotide 262. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:114 from nucleotide 91 to nucleotide 262, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:114 from nucleotide 91 to nucleotide 262, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:114 from nucleotide 91 to nucleotide 262.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:115;
  - (b) the amino acid sequence of SEQ ID NO:115 from amino acid 1 to amino acid 66;
  - (c) a fragment of the amino acid sequence of SEQ ID NO:115, the fragment comprising eight contiguous amino acids of SEQ ID NO:115; and
  - (d) the amino acid sequence encoded by the cDNA insert of clone AT340\_1 deposited with the ATCC under accession number 98271;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:115 or the amino acid sequence of SEQ ID NO:115 from amino acid 1 to amino acid 66. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:115 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:115, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:115 having biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID NO:115.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:116;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:116 from nucleotide 2 to nucleotide 601;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:116 from nucleotide 401 to nucleotide 601;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BG132\_1 deposited with the ATCC under accession number 98271;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BG132\_1 deposited with the ATCC under accession number 98271;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BG132\_1 deposited with the ATCC under accession number 98271;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BG132\_1 deposited with the ATCC under accession number 98271;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:117;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:117 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:117;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:116.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:116 from nucleotide 2 to nucleotide 601; the nucleotide sequence of SEQ ID NO:116 from nucleotide 401 to nucleotide 601; the nucleotide sequence of the full-length protein coding sequence of clone BG132\_1 deposited with the ATCC under accession number 98271; or the nucleotide sequence of a mature protein coding sequence of clone BG132\_1 deposited with the ATCC under accession number 98271. In other preferred embodiments, the polynucleotide encodes the full-length or a



mature protein encoded by the cDNA insert of clone BG132\_1 deposited with the ATCC under accession number 98271. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:117 from amino acid 119 to amino acid 200. In further preferred embodiments, the present invention  
5 provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:117 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:117, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:117 having biological activity, the fragment comprising the amino acid sequence from amino  
10 acid 95 to amino acid 104 of SEQ ID NO:117.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:116 and SEQ ID NO:118.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:116;
    - 20 (ab) SEQ ID NO:118, but excluding the poly(A) tail at the 3' end of SEQ ID NO:118; and
    - (ac) the nucleotide sequence of the cDNA insert of clone BG132\_1 deposited with the ATCC under accession number 98271;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions  
25 at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in  
30 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:116;
    - (bb) SEQ ID NO:118, but excluding the poly(A) tail at the 3' end of SEQ ID NO:118; and

- (bc) the nucleotide sequence of the cDNA insert of clone BG132\_1 deposited with the ATCC under accession number 98271;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:116 and SEQ ID NO:118, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:116 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:118, but excluding the poly(A) tail at the 3' end of SEQ ID NO:118. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:116, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:116 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:116. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:116 from nucleotide 2 to nucleotide 601, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:116 from nucleotide 2 to nucleotide 601, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:116 from nucleotide 2 to nucleotide 601. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:116 from nucleotide 401 to nucleotide 601, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:116 from nucleotide 401 to nucleotide 601, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:116 from nucleotide 401 to nucleotide 601.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:117;
- (b) the amino acid sequence of SEQ ID NO:117 from amino acid 119 to amino acid 200;
- 30 (c) a fragment of the amino acid sequence of SEQ ID NO:117, the fragment comprising eight contiguous amino acids of SEQ ID NO:117; and
- (d) the amino acid sequence encoded by the cDNA insert of clone BG132\_1 deposited with the ATCC under accession number 98271;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:117 or the amino acid sequence of SEQ ID NO:117 from amino acid 119 to amino acid 200. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:117 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:117, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:117 having biological activity, the fragment comprising the amino acid sequence from amino acid 95 to amino acid 104 of SEQ ID NO:117.

10 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:119;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:119 from nucleotide 225 to nucleotide 701;
- 15 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BG219\_2 deposited with the ATCC under accession number 98271;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BG219\_2 deposited with the ATCC under accession number 98271;
- 20 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BG219\_2 deposited with the ATCC under accession number 98271;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BG219\_2 deposited with the ATCC under accession number 98271;
- 25 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:120;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:120;
- 30 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of
- 35 the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:119.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:119  
5 from nucleotide 225 to nucleotide 701; the nucleotide sequence of the full-length protein coding sequence of clone BG219\_2 deposited with the ATCC under accession number 98271; or the nucleotide sequence of a mature protein coding sequence of clone BG219\_2 deposited with the ATCC under accession number 98271. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BG219\_2  
10 deposited with the ATCC under accession number 98271. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:120 from amino acid 1 to amino acid 97. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the fragment  
15 preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:120, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the fragment comprising the amino acid sequence from amino acid 74 to amino acid 83 of SEQ ID NO:120.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID  
20 NO:119.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X  
25 SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:119, but excluding the poly(A) tail at the 3' end of SEQ ID NO:119; and
    - (ab) the nucleotide sequence of the cDNA insert of clone  
30 BG219\_2 deposited with the ATCC under accession number 98271;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- 35 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:119, but excluding the poly(A) tail at the 3' end of SEQ ID NO:119; and

(bb) the nucleotide sequence of the cDNA insert of clone BG219\_2 deposited with the ATCC under accession number 98271;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

10 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:119, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:119 to a nucleotide  
15 sequence corresponding to the 3' end of SEQ ID NO:119, but excluding the poly(A) tail at the 3' end of SEQ ID NO:119. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:119 from nucleotide 225 to nucleotide 701, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:119 from nucleotide 225 to nucleotide  
20 701, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:119 from nucleotide 225 to nucleotide 701.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:120;  
25 (b) the amino acid sequence of SEQ ID NO:120 from amino acid 1 to amino acid 97;

(c) a fragment of the amino acid sequence of SEQ ID NO:120, the fragment comprising eight contiguous amino acids of SEQ ID NO:120; and

(d) the amino acid sequence encoded by the cDNA insert of clone BG219\_2  
30 deposited with the ATCC under accession number 98271;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:120 or the amino acid sequence of SEQ ID NO:120 from amino acid 1 to amino acid 97. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID  
35 NO:120 having biological activity, the fragment preferably comprising eight (more preferably

twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:120, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the fragment comprising the amino acid sequence from amino acid 74 to amino acid 83 of SEQ ID NO:120.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:121;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:121 from nucleotide 2115 to nucleotide 2510;
- 10 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:121 from nucleotide 1 to nucleotide 324;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BG366\_2 deposited with the ATCC under accession number 98271;
- 15 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BG366\_2 deposited with the ATCC under accession number 98271;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BG366\_2 deposited with the ATCC under accession number 98271;
- 20 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BG366\_2 deposited with the ATCC under accession number 98271;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:122;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:122;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:121.
- 35

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:121 from nucleotide 2115 to nucleotide 2510; the nucleotide sequence of SEQ ID NO:121 from nucleotide 1 to nucleotide 324; the nucleotide sequence of the full-length protein coding sequence of clone BG366\_2 deposited with the ATCC under accession number 98271; or the nucleotide  
5 sequence of a mature protein coding sequence of clone BG366\_2 deposited with the ATCC under accession number 98271. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BG366\_2 deposited with the ATCC under accession number 98271. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence  
10 of SEQ ID NO:122 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:122, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:122.

15 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:121.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - 20 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:121, but excluding the poly(A) tail at the 3' end of SEQ ID NO:121; and
    - 25 (ab) the nucleotide sequence of the cDNA insert of clone BG366\_2 deposited with the ATCC under accession number 98271;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
  - 30 and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:121, but excluding the poly(A) tail at the 3' end of SEQ ID NO:121; and

(bb) the nucleotide sequence of the cDNA insert of clone BG366\_2 deposited with the ATCC under accession number 98271;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide  
10 sequence corresponding to the cDNA sequence of SEQ ID NO:121, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:121 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:121, but excluding the poly(A) tail at the 3' end of SEQ ID NO:121. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:121  
15 from nucleotide 2115 to nucleotide 2510, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:121 from nucleotide 2115 to nucleotide 2510, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:121 from nucleotide 2115 to nucleotide 2510. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA  
20 sequence of SEQ ID NO:121 from nucleotide 1 to nucleotide 324, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:121 from nucleotide 1 to nucleotide 324, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:121 from nucleotide 1 to nucleotide 324.

In other embodiments, the present invention provides a composition comprising a protein,  
25 wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:122;

(b) a fragment of the amino acid sequence of SEQ ID NO:122, the fragment comprising eight contiguous amino acids of SEQ ID NO:122; and

(c) the amino acid sequence encoded by the cDNA insert of clone BG366\_2  
30 deposited with the ATCC under accession number 98271;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:122. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment preferably comprising eight (more preferably  
35 twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:122, or a protein



comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:122.

- In one embodiment, the present invention provides a composition comprising an isolated
- 5 polynucleotide selected from the group consisting of:
- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:123;
  - (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:123 from nucleotide 27 to nucleotide 215;
  - (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:123  
10 from nucleotide 27 to nucleotide 181;
  - (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BV172\_2 deposited with the ATCC under accession number 98271;
  - (e) a polynucleotide encoding the full-length protein encoded by the cDNA  
15 insert of clone BV172\_2 deposited with the ATCC under accession number 98271;
  - (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BV172\_2 deposited with the ATCC under accession number 98271;
  - (g) a polynucleotide encoding a mature protein encoded by the cDNA insert  
20 of clone BV172\_2 deposited with the ATCC under accession number 98271;
  - (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:124;
  - (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment comprising  
25 eight contiguous amino acids of SEQ ID NO:124;
  - (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
  - (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
  - (l) a polynucleotide that hybridizes under stringent conditions to any one of  
30 the polynucleotides specified in (a)-(i); and
  - (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:123.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:123 from nucleotide 27 to nucleotide 215; the nucleotide sequence of SEQ ID NO:123 from nucleotide 27 to nucleotide 181; the nucleotide sequence of the full-length protein coding sequence of clone BV172\_2 deposited with the ATCC under accession number 98271; or the

5 nucleotide sequence of a mature protein coding sequence of clone BV172\_2 deposited with the ATCC under accession number 98271. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BV172\_2 deposited with the ATCC under accession number 98271. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid

10 sequence of SEQ ID NO:124 from amino acid 1 to amino acid 51. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:124, or a polynucleotide encoding a protein comprising a fragment of the

15 amino acid sequence of SEQ ID NO:124 having biological activity, the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID NO:124.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:123.

Further embodiments of the invention provide isolated polynucleotides produced

20 according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
    - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
      - 25 (aa) SEQ ID NO:123, but excluding the poly(A) tail at the 3' end of SEQ ID NO:123; and
      - (ab) the nucleotide sequence of the cDNA insert of clone BV172\_2 deposited with the ATCC under accession number 98271;
      - (ii) hybridizing said probe(s) to human genomic DNA in conditions
      - 30 at least as stringent as 4X SSC at 50 degrees C; and
      - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:123, but excluding the poly(A) tail at the 3' end of SEQ ID NO:123; and

(bb) the nucleotide sequence of the cDNA insert of clone BV172\_2 deposited with the ATCC under accession number 98271;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

10 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:123, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:123 to a nucleotide  
15 sequence corresponding to the 3' end of SEQ ID NO:123, but excluding the poly(A) tail at the 3' end of SEQ ID NO:123. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:123 from nucleotide 27 to nucleotide 215, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:123 from nucleotide 27 to nucleotide  
20 215, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:123 from nucleotide 27 to nucleotide 215. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:123 from nucleotide 27 to nucleotide 181, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:123 from nucleotide 27 to  
25 nucleotide 181, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:123 from nucleotide 27 to nucleotide 181.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:124;  
30 (b) the amino acid sequence of SEQ ID NO:124 from amino acid 1 to amino acid 51;

(c) a fragment of the amino acid sequence of SEQ ID NO:124, the fragment comprising eight contiguous amino acids of SEQ ID NO:124; and

(d) the amino acid sequence encoded by the cDNA insert of clone BV172\_2  
35 deposited with the ATCC under accession number 98271;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:124 or the amino acid sequence of SEQ ID NO:124 from amino acid 1 to amino acid 51. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:124, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID NO:124.

10 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:125;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:125 from nucleotide 338 to nucleotide 409;
- 15 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:125 from nucleotide 362 to nucleotide 409;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:125 from nucleotide 270 to nucleotide 419;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CC247\_10 deposited with the ATCC under accession number 98271;
- 20 (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CC247\_10 deposited with the ATCC under accession number 98271;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CC247\_10 deposited with the ATCC under accession number 98271;
- 25 (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CC247\_10 deposited with the ATCC under accession number 98271;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:126;
- 30 (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:126;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h)
- 35 above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

5 (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:125.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:125 from nucleotide 338 to nucleotide 409; the nucleotide sequence of SEQ ID NO:125 from  
10 nucleotide 362 to nucleotide 409; the nucleotide sequence of SEQ ID NO:125 from nucleotide 270 to nucleotide 419; the nucleotide sequence of the full-length protein coding sequence of clone CC247\_10 deposited with the ATCC under accession number 98271; or the nucleotide sequence of a mature protein coding sequence of clone CC247\_10 deposited with the ATCC under accession number 98271. In other preferred embodiments, the polynucleotide encodes the full-  
15 length or a mature protein encoded by the cDNA insert of clone CC247\_10 deposited with the ATCC under accession number 98271. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:126, or a  
20 polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment comprising the amino acid sequence from amino acid 7 to amino acid 16 of SEQ ID NO:126.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:125.

25 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting  
30 of:

(aa) SEQ ID NO:125, but excluding the poly(A) tail at the 3' end of SEQ ID NO:125; and

(ab) the nucleotide sequence of the cDNA insert of clone CC247\_10 deposited with the ATCC under accession number 98271;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

5 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:125, but excluding the poly(A) tail at the 3' end of SEQ ID NO:125; and

(bb) the nucleotide sequence of the cDNA insert of clone CC247\_10 deposited with the ATCC under accession number 98271;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

15 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:125, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:125 to a nucleotide  
20 sequence corresponding to the 3' end of SEQ ID NO:125, but excluding the poly(A) tail at the 3' end of SEQ ID NO:125. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:125 from nucleotide 338 to nucleotide 409, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:125 from nucleotide 338 to nucleotide  
25 409, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:125 from nucleotide 338 to nucleotide 409. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:125 from nucleotide 362 to nucleotide 409, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:125 from nucleotide 362  
30 to nucleotide 409, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:125 from nucleotide 362 to nucleotide 409. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:125 from nucleotide 270 to nucleotide 419, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:125 from

nucleotide 270 to nucleotide 419, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:125 from nucleotide 270 to nucleotide 419.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 5                   (a)     the amino acid sequence of SEQ ID NO:126;
- (b)     a fragment of the amino acid sequence of SEQ ID NO:126, the fragment comprising eight contiguous amino acids of SEQ ID NO:126; and
- (c)     the amino acid sequence encoded by the cDNA insert of clone CC247\_10 deposited with the ATCC under accession number 98271;
- 10   the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:126. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:126, or a protein
- 15   comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment comprising the amino acid sequence from amino acid 7 to amino acid 16 of SEQ ID NO:126.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 20                   (a)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:127;
- (b)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:127 from nucleotide 128 to nucleotide 1600;
- (c)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:127 from nucleotide 281 to nucleotide 1600;
- 25                   (d)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:127 from nucleotide 62 to nucleotide 373;
- (e)     a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CI480\_9 deposited with the ATCC under accession number 98271;
- 30                   (f)     a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CI480\_9 deposited with the ATCC under accession number 98271;
- (g)     a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CI480\_9 deposited with the ATCC under accession number 98271;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CI480\_9 deposited with the ATCC under accession number 98271;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:128;

5 (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:128;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

10 (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of  
15 the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:127.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:127 from nucleotide 128 to nucleotide 1600; the nucleotide sequence of SEQ ID NO:127 from nucleotide 281 to nucleotide 1600; the nucleotide sequence of SEQ ID NO:127 from nucleotide  
20 62 to nucleotide 373; the nucleotide sequence of the full-length protein coding sequence of clone CI480\_9 deposited with the ATCC under accession number 98271; or the nucleotide sequence of a mature protein coding sequence of clone CI480\_9 deposited with the ATCC under accession number 98271. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CI480\_9 deposited with the ATCC under  
25 accession number 98271. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:128 from amino acid 1 to amino acid 82. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment preferably comprising eight (more preferably  
30 twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:128, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment comprising the amino acid sequence from amino acid 240 to amino acid 249 of SEQ ID NO:128.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID  
35 NO:127.



Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:127, but excluding the poly(A) tail at the 3' end of SEQ ID NO:127; and

(ab) the nucleotide sequence of the cDNA insert of clone CI480\_9 deposited with the ATCC under accession number 98271;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:127, but excluding the poly(A) tail at the 3' end of SEQ ID NO:127; and

(bb) the nucleotide sequence of the cDNA insert of clone CI480\_9 deposited with the ATCC under accession number 98271;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:127, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:127 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:127, but excluding the poly(A) tail at the 3' end of SEQ ID NO:127. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:127 from nucleotide 128 to nucleotide 1600, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:127 from nucleotide 128 to nucleotide 1600, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:127

from nucleotide 128 to nucleotide 1600. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:127 from nucleotide 281 to nucleotide 1600, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:127 from  
5 nucleotide 281 to nucleotide 1600, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:127 from nucleotide 281 to nucleotide 1600. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:127 from nucleotide 62 to nucleotide 373, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said  
10 sequence of SEQ ID NO:127 from nucleotide 62 to nucleotide 373, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:127 from nucleotide 62 to nucleotide 373.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:128;
- (b) the amino acid sequence of SEQ ID NO:128 from amino acid 1 to amino acid 82;
- (c) a fragment of the amino acid sequence of SEQ ID NO:128, the fragment comprising eight contiguous amino acids of SEQ ID NO:128; and
- 20 (d) the amino acid sequence encoded by the cDNA insert of clone CI480\_9 deposited with the ATCC under accession number 98271;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:128 or the amino acid sequence of SEQ ID NO:128 from amino acid 1 to amino acid 82. In further preferred embodiments, the present  
25 invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:128, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment comprising the amino acid sequence from amino acid 240 to amino acid 249 of SEQ  
30 ID NO:128.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:129;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:129  
35 from nucleotide 383 to nucleotide 3958;

- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:129 from nucleotide 470 to nucleotide 3958;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:129 from nucleotide 271 to nucleotide 488;
- 5 (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CO722\_1 deposited with the ATCC under accession number 98271;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CO722\_1 deposited with the ATCC under accession number 98271;
- 10 (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CO722\_1 deposited with the ATCC under accession number 98271;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CO722\_1 deposited with the ATCC under accession number 98271;
- 15 (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:130;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:130;
- 20 (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- 25 (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:129.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:129 from nucleotide 383 to nucleotide 3958; the nucleotide sequence of SEQ ID NO:129 from nucleotide 470 to nucleotide 3958; the nucleotide sequence of SEQ ID NO:129 from nucleotide 271 to nucleotide 488; the nucleotide sequence of the full-length protein coding sequence of clone CO722\_1 deposited with the ATCC under accession number 98271; or the nucleotide sequence of a mature protein coding sequence of clone CO722\_1 deposited with the ATCC under accession number 98271. In other preferred embodiments, the polynucleotide encodes the full-length or a

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mature protein encoded by the cDNA insert of clone CO722\_1 deposited with the ATCC under accession number 98271. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:130 from amino acid 1 to amino acid 34. In further preferred embodiments, the present invention provides  
5 a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:130, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment comprising the amino acid sequence from amino acid 591 to  
10 amino acid 600 of SEQ ID NO:130.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:129.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:129, but excluding the poly(A) tail at the 3'  
20 end of SEQ ID NO:129; and
    - (ab) the nucleotide sequence of the cDNA insert of clone CO722\_1 deposited with the ATCC under accession number 98271;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - 25 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group  
30 consisting of:
    - (ba) SEQ ID NO:129, but excluding the poly(A) tail at the 3' end of SEQ ID NO:129; and
    - (bb) the nucleotide sequence of the cDNA insert of clone CO722\_1 deposited with the ATCC under accession number 98271;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:129, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:129 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:129, but excluding the poly(A) tail at the 3' end of SEQ ID NO:129. Also preferably the polynucleotide isolated according to the above  
10 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:129 from nucleotide 383 to nucleotide 3958, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:129 from nucleotide 383 to nucleotide 3958, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:129 from nucleotide 383 to nucleotide 3958. Also preferably the polynucleotide isolated according  
15 to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:129 from nucleotide 470 to nucleotide 3958, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:129 from nucleotide 470 to nucleotide 3958, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:129 from nucleotide 470 to nucleotide 3958. Also preferably the  
20 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:129 from nucleotide 271 to nucleotide 488, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:129 from nucleotide 271 to nucleotide 488, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:129 from nucleotide 271 to nucleotide  
25 488.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:130;
- (b) the amino acid sequence of SEQ ID NO:130 from amino acid 1 to amino  
30 acid 34;
- (c) a fragment of the amino acid sequence of SEQ ID NO:130, the fragment comprising eight contiguous amino acids of SEQ ID NO:130; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CO722\_1 deposited with the ATCC under accession number 98271;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:130 or the amino acid sequence of SEQ ID NO:130 from amino acid 1 to amino acid 34. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:130, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment comprising the amino acid sequence from amino acid 591 to amino acid 600 of SEQ ID NO:130.

10 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:131;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:131 from nucleotide 914 to nucleotide 2353;
- 15 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:131 from nucleotide 1793 to nucleotide 2353;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:131 from nucleotide 1037 to nucleotide 1260;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CT748\_2 deposited with the ATCC under accession number 98271;
- 20 (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CT748\_2 deposited with the ATCC under accession number 98271;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CT748\_2 deposited with the ATCC under accession number 98271;
- 25 (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CT748\_2 deposited with the ATCC under accession number 98271;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:132;
- 30 (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:132;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h)
- 35 above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

5 (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:131.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:131 from nucleotide 914 to nucleotide 2353; the nucleotide sequence of SEQ ID NO:131 from  
10 nucleotide 1793 to nucleotide 2353; the nucleotide sequence of SEQ ID NO:131 from nucleotide 1037 to nucleotide 1260; the nucleotide sequence of the full-length protein coding sequence of clone CT748\_2 deposited with the ATCC under accession number 98271; or the nucleotide sequence of a mature protein coding sequence of clone CT748\_2 deposited with the ATCC under accession number 98271. In other preferred embodiments, the polynucleotide encodes the full-  
15 length or a mature protein encoded by the cDNA insert of clone CT748\_2 deposited with the ATCC under accession number 98271. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:132 from amino acid 22 to amino acid 116. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid  
20 sequence of SEQ ID NO:132 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:132, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment comprising the amino acid sequence from amino acid 234 to amino acid 243 of SEQ ID NO:132.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:131.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:131, but excluding the poly(A) tail at the 3' end of SEQ ID NO:131; and

- (ab) the nucleotide sequence of the cDNA insert of clone CT748\_2 deposited with the ATCC under accession number 98271;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
- 10 consisting of:
- (ba) SEQ ID NO:131, but excluding the poly(A) tail at the 3' end of SEQ ID NO:131; and
- (bb) the nucleotide sequence of the cDNA insert of clone CT748\_2 deposited with the ATCC under accession number 98271;
- 15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- Preferably the polynucleotide isolated according to the above process comprises a nucleotide
- 20 sequence corresponding to the cDNA sequence of SEQ ID NO:131, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:131 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:131, but excluding the poly(A) tail at the 3' end of SEQ ID NO:131. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:131
- 25 from nucleotide 914 to nucleotide 2353, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:131 from nucleotide 914 to nucleotide 2353, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:131 from nucleotide 914 to nucleotide 2353. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of
- 30 SEQ ID NO:131 from nucleotide 1793 to nucleotide 2353, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:131 from nucleotide 1793 to nucleotide 2353, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:131 from nucleotide 1793 to nucleotide 2353. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence
- 35 corresponding to the cDNA sequence of SEQ ID NO:131 from nucleotide 1037 to nucleotide



1260, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:131 from nucleotide 1037 to nucleotide 1260, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:131 from nucleotide 1037 to nucleotide 1260.

5           In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a)     the amino acid sequence of SEQ ID NO:132;
- (b)     the amino acid sequence of SEQ ID NO:132 from amino acid 22 to amino acid 116;
- 10       (c)     a fragment of the amino acid sequence of SEQ ID NO:132, the fragment comprising eight contiguous amino acids of SEQ ID NO:132; and
- (d)     the amino acid sequence encoded by the cDNA insert of clone CT748\_2 deposited with the ATCC under accession number 98271;

the protein being substantially free from other mammalian proteins. Preferably such protein  
15       comprises the amino acid sequence of SEQ ID NO:132 or the amino acid sequence of SEQ ID NO:132 from amino acid 22 to amino acid 116. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:132, or a protein  
20       comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment comprising the amino acid sequence from amino acid 234 to amino acid 243 of SEQ ID NO:132.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25       (a)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:133;
- (b)     a polynucleotide comprising the nucleotide sequence of SEQ ID NO:133 from nucleotide 22 to nucleotide 462;
- (c)     a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AJ1\_1 deposited with the ATCC under accession  
30       number 98278;
- (d)     a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AJ1\_1 deposited with the ATCC under accession number 98278;
- (e)     a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AJ1\_1 deposited with the ATCC under accession number  
35       98278;

- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AJ1\_1 deposited with the ATCC under accession number 98278;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:134;
- 5 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:134;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 10 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:133.
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Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:133 from nucleotide 22 to nucleotide 462; the nucleotide sequence of the full-length protein coding sequence of clone AJ1\_1 deposited with the ATCC under accession number 98278; or the nucleotide sequence of a mature protein coding sequence of clone AJ1\_1 deposited with the ATCC under accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AJ1\_1 deposited with the ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:134 from amino acid 52 to amino acid 147. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:134, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment comprising the amino acid sequence from amino acid 68 to amino acid 77 of SEQ ID NO:134.

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Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:133 and SEQ ID NO:135.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

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- (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:133;
    - (ab) SEQ ID NO:135, but excluding the poly(A) tail at the 3' end of SEQ ID NO:135; and
    - (ac) the nucleotide sequence of the cDNA insert of clone AJ1\_1 deposited with the ATCC under accession number 98278;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:133;
    - (bb) SEQ ID NO:135, but excluding the poly(A) tail at the 3' end of SEQ ID NO:135; and
    - (bc) the nucleotide sequence of the cDNA insert of clone AJ1\_1 deposited with the ATCC under accession number 98278;
  - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
  - (iii) amplifying human DNA sequences; and
  - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:133 and SEQ ID NO:135, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:133 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:135, but excluding the poly(A) tail at the 3' end of SEQ ID NO:135. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:133, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:133 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:133. Also preferably the polynucleotide isolated according to the above

process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:133 from nucleotide 22 to nucleotide 462, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:133 from nucleotide 22 to nucleotide 462, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:133 from nucleotide 22 to nucleotide 462.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:134;
  - (b) the amino acid sequence of SEQ ID NO:134 from amino acid 52 to amino acid 147;
  - (c) a fragment of the amino acid sequence of SEQ ID NO:134, the fragment comprising eight contiguous amino acids of SEQ ID NO:134; and
  - (d) the amino acid sequence encoded by the cDNA insert of clone AJ1\_1 deposited with the ATCC under accession number 98278;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:134 or the amino acid sequence of SEQ ID NO:134 from amino acid 52 to amino acid 147. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:134, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment comprising the amino acid sequence from amino acid 68 to amino acid 77 of SEQ ID NO:134.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:136;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:136 from nucleotide 7 to nucleotide 1647;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:136 from nucleotide 1 to nucleotide 305;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AQ73\_3 deposited with the ATCC under accession number 98278;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AQ73\_3 deposited with the ATCC under accession number 98278;

- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AQ73\_3 deposited with the ATCC under accession number 98278;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert  
5 of clone AQ73\_3 deposited with the ATCC under accession number 98278;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:137;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:137 having biological activity, the fragment comprising  
10 eight contiguous amino acids of SEQ ID NO:137;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of  
15 the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:136.
- 20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:136 from nucleotide 7 to nucleotide 1647; the nucleotide sequence of SEQ ID NO:136 from nucleotide 1 to nucleotide 305; the nucleotide sequence of the full-length protein coding sequence of clone AQ73\_3 deposited with the ATCC under accession number 98278; or the nucleotide sequence of a mature protein coding sequence of clone AQ73\_3 deposited with the ATCC under  
25 accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AQ73\_3 deposited with the ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:137 from amino acid 1 to amino acid 68. In further preferred embodiments, the present  
30 invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:137 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:137, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:137 having biological activity, the fragment comprising the amino acid sequence from  
35 amino acid 268 to amino acid 277 of SEQ ID NO:137.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:136.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (aa) SEQ ID NO:136, but excluding the poly(A) tail at the 3' end of SEQ ID NO:136; and

(ab) the nucleotide sequence of the cDNA insert of clone AQ73\_3 deposited with the ATCC under accession number 98278;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:

20 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:136, but excluding the poly(A) tail at the 3' end of SEQ ID NO:136; and

(bb) the nucleotide sequence of the cDNA insert of clone AQ73\_3 deposited with the ATCC under accession number 98278;

25 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide  
30 sequence corresponding to the cDNA sequence of SEQ ID NO:136, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:136 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:136, but excluding the poly(A) tail at the 3' end of SEQ ID NO:136. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:136  
35 from nucleotide 7 to nucleotide 1647, and extending contiguously from a nucleotide sequence

corresponding to the 5' end of said sequence of SEQ ID NO:136 from nucleotide 7 to nucleotide 1647, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:136 from nucleotide 7 to nucleotide 1647. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ  
5 ID NO:136 from nucleotide 1 to nucleotide 305, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:136 from nucleotide 1 to nucleotide 305, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:136 from nucleotide 1 to nucleotide 305.

In other embodiments, the present invention provides a composition comprising a protein,  
10 wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:137;
- (b) the amino acid sequence of SEQ ID NO:137 from amino acid 1 to amino acid 68;
- (c) a fragment of the amino acid sequence of SEQ ID NO:137, the fragment  
15 comprising eight contiguous amino acids of SEQ ID NO:137; and
- (d) the amino acid sequence encoded by the cDNA insert of clone AQ73\_3 deposited with the ATCC under accession number 98278;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:137 or the amino acid sequence of SEQ ID  
20 NO:137 from amino acid 1 to amino acid 68. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:137 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:137, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:137 having biological activity,  
25 the fragment comprising the amino acid sequence from amino acid 268 to amino acid 277 of SEQ ID NO:137.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:138;
- 30 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:138 from nucleotide 62 to nucleotide 757;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:138 from nucleotide 357 to nucleotide 703;

- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BG142\_1 deposited with the ATCC under accession number 98278;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BG142\_1 deposited with the ATCC under accession number 98278;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BG142\_1 deposited with the ATCC under accession number 98278;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BG142\_1 deposited with the ATCC under accession number 98278;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:139;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:139 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:139;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:138.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:138 from nucleotide 62 to nucleotide 757; the nucleotide sequence of SEQ ID NO:138 from nucleotide 357 to nucleotide 703; the nucleotide sequence of the full-length protein coding sequence of clone BG142\_1 deposited with the ATCC under accession number 98278; or the nucleotide sequence of a mature protein coding sequence of clone BG142\_1 deposited with the ATCC under accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BG142\_1 deposited with the ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:139 from amino acid 184 to amino acid 214. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a



fragment of the amino acid sequence of SEQ ID NO:139 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:139, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:139 having biological activity, the fragment comprising the  
5 amino acid sequence from amino acid 111 to amino acid 120 of SEQ ID NO:139.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:138.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 10 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 15 (aa) SEQ ID NO:138, but excluding the poly(A) tail at the 3' end of SEQ ID NO:138; and
- (ab) the nucleotide sequence of the cDNA insert of clone BG142\_1 deposited with the ATCC under accession number 98278;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 20 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 25 (ba) SEQ ID NO:138, but excluding the poly(A) tail at the 3' end of SEQ ID NO:138; and
- (bb) the nucleotide sequence of the cDNA insert of clone BG142\_1 deposited with the ATCC under accession number 98278;
- 30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide  
35 sequence corresponding to the cDNA sequence of SEQ ID NO:138, and extending contiguously

from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:138 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:138, but excluding the poly(A) tail at the 3' end of SEQ ID NO:138. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:138  
5 from nucleotide 62 to nucleotide 757, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:138 from nucleotide 62 to nucleotide 757, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:138 from nucleotide 62 to nucleotide 757. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ  
10 ID NO:138 from nucleotide 357 to nucleotide 703, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:138 from nucleotide 357 to nucleotide 703, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:138 from nucleotide 357 to nucleotide 703.

In other embodiments, the present invention provides a composition comprising a protein,  
15 wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:139;
- (b) the amino acid sequence of SEQ ID NO:139 from amino acid 184 to amino acid 214;
- (c) a fragment of the amino acid sequence of SEQ ID NO:139, the fragment  
20 comprising eight contiguous amino acids of SEQ ID NO:139; and
- (d) the amino acid sequence encoded by the cDNA insert of clone BG142\_1 deposited with the ATCC under accession number 98278;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:139 or the amino acid sequence of SEQ ID  
25 NO:139 from amino acid 184 to amino acid 214. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:139 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:139, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:139 having biological activity,  
30 the fragment comprising the amino acid sequence from amino acid 111 to amino acid 120 of SEQ ID NO:139.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:140;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:140 from nucleotide 404 to nucleotide 535;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:140 from nucleotide 1 to nucleotide 666;
- 5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BV66\_1 deposited with the ATCC under accession number 98278;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BV66\_1 deposited with the ATCC under accession number 98278;
- 10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BV66\_1 deposited with the ATCC under accession number 98278;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BV66\_1 deposited with the ATCC under accession number 98278;
- 15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:141;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:141 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:141;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 25 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:140.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:140 from nucleotide 404 to nucleotide 535; the nucleotide sequence of SEQ ID NO:140 from nucleotide 1 to nucleotide 666; the nucleotide sequence of the full-length protein coding sequence of clone BV66\_1 deposited with the ATCC under accession number 98278; or the nucleotide sequence of a mature protein coding sequence of clone BV66\_1 deposited with the ATCC under accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BV66\_1 deposited with the

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ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:141 from amino acid 1 to amino acid 38. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid  
5 sequence of SEQ ID NO:141 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:141, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:141 having biological activity, the fragment comprising the amino acid sequence from amino acid 17 to amino acid 26 of SEQ ID NO:141.

10 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:140.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - 15 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:140, but excluding the poly(A) tail at the 3' end of SEQ ID NO:140; and
    - 20 (ab) the nucleotide sequence of the cDNA insert of clone BV66\_1 deposited with the ATCC under accession number 98278;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
  - 25 and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 30 (ba) SEQ ID NO:140, but excluding the poly(A) tail at the 3' end of SEQ ID NO:140; and
    - (bb) the nucleotide sequence of the cDNA insert of clone BV66\_1 deposited with the ATCC under accession number 98278;
    - (ii) hybridizing said primer(s) to human genomic DNA in conditions
    - 35 at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:140, and extending contiguously  
5 from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:140 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:140, but excluding the poly(A) tail at the 3' end of SEQ ID NO:140. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:140 from nucleotide 404 to nucleotide 535, and extending contiguously from a nucleotide sequence  
10 corresponding to the 5' end of said sequence of SEQ ID NO:140 from nucleotide 404 to nucleotide 535, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:140 from nucleotide 404 to nucleotide 535. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:140 from nucleotide 1 to nucleotide 666, and extending contiguously from a nucleotide  
15 sequence corresponding to the 5' end of said sequence of SEQ ID NO:140 from nucleotide 1 to nucleotide 666, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:140 from nucleotide 1 to nucleotide 666.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:141;
- (b) the amino acid sequence of SEQ ID NO:141 from amino acid 1 to amino acid 38;
- (c) a fragment of the amino acid sequence of SEQ ID NO:141, the fragment comprising eight contiguous amino acids of SEQ ID NO:141; and
- 25 (d) the amino acid sequence encoded by the cDNA insert of clone BV66\_1 deposited with the ATCC under accession number 98278;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:141 or the amino acid sequence of SEQ ID NO:141 from amino acid 1 to amino acid 38. In further preferred embodiments, the present  
30 invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:141 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:141, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:141 having biological activity, the fragment comprising the amino acid sequence from amino acid 17 to amino acid 26 of SEQ  
35 ID NO:141.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:142;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:142  
5 from nucleotide 1204 to nucleotide 1389;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:142  
from nucleotide 881 to nucleotide 1380;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length  
protein coding sequence of clone BV291\_3 deposited with the ATCC under accession  
10 number 98278;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA  
insert of clone BV291\_3 deposited with the ATCC under accession number 98278;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein  
coding sequence of clone BV291\_3 deposited with the ATCC under accession number  
15 98278;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert  
of clone BV291\_3 deposited with the ATCC under accession number 98278;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence  
of SEQ ID NO:143;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino  
20 acid sequence of SEQ ID NO:143 having biological activity, the fragment comprising  
eight contiguous amino acids of SEQ ID NO:143;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g)  
above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h)  
25 or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of  
the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of  
30 the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the  
length of SEQ ID NO:142.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:142  
from nucleotide 1204 to nucleotide 1389; the nucleotide sequence of SEQ ID NO:142 from  
nucleotide 881 to nucleotide 1380; the nucleotide sequence of the full-length protein coding  
35 sequence of clone BV291\_3 deposited with the ATCC under accession number 98278; or the

nucleotide sequence of a mature protein coding sequence of clone BV291\_3 deposited with the ATCC under accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BV291\_3 deposited with the ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:143 from amino acid 1 to amino acid 59. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:143 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:143, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:143 having biological activity, the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID NO:143.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:142.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:142, but excluding the poly(A) tail at the 3' end of SEQ ID NO:142; and

(ab) the nucleotide sequence of the cDNA insert of clone BV291\_3 deposited with the ATCC under accession number 98278;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:142, but excluding the poly(A) tail at the 3' end of SEQ ID NO:142; and

- (bb) the nucleotide sequence of the cDNA insert of clone BV291\_3 deposited with the ATCC under accession number 98278;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:142, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:142 to a nucleotide  
10 sequence corresponding to the 3' end of SEQ ID NO:142, but excluding the poly(A) tail at the 3' end of SEQ ID NO:142. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:142 from nucleotide 1204 to nucleotide 1389, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:142 from nucleotide 1204 to  
15 nucleotide 1389, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:142 from nucleotide 1204 to nucleotide 1389. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:142 from nucleotide 881 to nucleotide 1380, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:142 from  
20 nucleotide 881 to nucleotide 1380, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:142 from nucleotide 881 to nucleotide 1380.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:143;
- 25 (b) the amino acid sequence of SEQ ID NO:143 from amino acid 1 to amino acid 59;
- (c) a fragment of the amino acid sequence of SEQ ID NO:143, the fragment comprising eight contiguous amino acids of SEQ ID NO:143; and
- (d) the amino acid sequence encoded by the cDNA insert of clone BV291\_3  
30 deposited with the ATCC under accession number 98278;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:143 or the amino acid sequence of SEQ ID NO:143 from amino acid 1 to amino acid 59. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID  
35 NO:143 having biological activity, the fragment preferably comprising eight (more preferably



twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:143, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:143 having biological activity, the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID NO:143.

5           In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:144;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:144 from nucleotide 189 to nucleotide 1115;
- 10           (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:144 from nucleotide 1 to nucleotide 451;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CK201\_1 deposited with the ATCC under accession number 98278;
- 15           (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CK201\_1 deposited with the ATCC under accession number 98278;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CK201\_1 deposited with the ATCC under accession number 98278;
- 20           (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CK201\_1 deposited with the ATCC under accession number 98278;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:145;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:145 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:145;
- 25           (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30           (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:144.
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Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:144 from nucleotide 189 to nucleotide 1115; the nucleotide sequence of SEQ ID NO:144 from nucleotide 1 to nucleotide 451; the nucleotide sequence of the full-length protein coding sequence of clone CK201\_1 deposited with the ATCC under accession number 98278; or the nucleotide  
5 sequence of a mature protein coding sequence of clone CK201\_1 deposited with the ATCC under accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CK201\_1 deposited with the ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID  
10 NO:145 from amino acid 1 to amino acid 88. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:145 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:145, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ  
15 ID NO:145 having biological activity, the fragment comprising the amino acid sequence from amino acid 149 to amino acid 158 of SEQ ID NO:145.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:144.

Further embodiments of the invention provide isolated polynucleotides produced  
20 according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 25 (aa) SEQ ID NO:144, but excluding the poly(A) tail at the 3' end of SEQ ID NO:144; and
    - (ab) the nucleotide sequence of the cDNA insert of clone CK201\_1 deposited with the ATCC under accession number 98278;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions  
30 at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

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(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:144, but excluding the poly(A) tail at the 3' end of SEQ ID NO:144; and

(bb) the nucleotide sequence of the cDNA insert of clone CK201\_1 deposited with the ATCC under accession number 98278;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

10 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:144, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:144 to a nucleotide  
15 sequence corresponding to the 3' end of SEQ ID NO:144, but excluding the poly(A) tail at the 3' end of SEQ ID NO:144. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:144 from nucleotide 189 to nucleotide 1115, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:144 from nucleotide 189 to nucleotide  
20 1115, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:144 from nucleotide 189 to nucleotide 1115. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:144 from nucleotide 1 to nucleotide 451, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:144 from  
25 nucleotide 1 to nucleotide 451, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:144 from nucleotide 1 to nucleotide 451.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:145;  
30 (b) the amino acid sequence of SEQ ID NO:145 from amino acid 1 to amino acid 88;

(c) a fragment of the amino acid sequence of SEQ ID NO:145, the fragment comprising eight contiguous amino acids of SEQ ID NO:145; and

(d) the amino acid sequence encoded by the cDNA insert of clone CK201\_1  
35 deposited with the ATCC under accession number 98278;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:145 or the amino acid sequence of SEQ ID NO:145 from amino acid 1 to amino acid 88. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:145 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:145, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:145 having biological activity, the fragment comprising the amino acid sequence from amino acid 149 to amino acid 158 of SEQ ID NO:145.

10 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:146;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:146 from nucleotide 117 to nucleotide 923;
- 15 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:146 from nucleotide 174 to nucleotide 923;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:146 from nucleotide 1 to nucleotide 316;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CQ331\_2 deposited with the ATCC under accession number 98278;
- 20 (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CQ331\_2 deposited with the ATCC under accession number 98278;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CQ331\_2 deposited with the ATCC under accession number 98278;
- 25 (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CQ331\_2 deposited with the ATCC under accession number 98278;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:147;
- 30 (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:147 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:147;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h)
- 35 above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

5 (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:146.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:146 from nucleotide 117 to nucleotide 923; the nucleotide sequence of SEQ ID NO:146 from  
10 nucleotide 174 to nucleotide 923; the nucleotide sequence of SEQ ID NO:146 from nucleotide 1 to nucleotide 316; the nucleotide sequence of the full-length protein coding sequence of clone CQ331\_2 deposited with the ATCC under accession number 98278; or the nucleotide sequence of a mature protein coding sequence of clone CQ331\_2 deposited with the ATCC under accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a  
15 mature protein encoded by the cDNA insert of clone CQ331\_2 deposited with the ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:147 from amino acid 1 to amino acid 57. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ  
20 ID NO:147 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:147, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:147 having biological activity, the fragment comprising the amino acid sequence from amino acid 129 to amino acid 138 of SEQ ID NO:147.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:146.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:  
30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:146, but excluding the poly(A) tail at the 3' end of SEQ ID NO:146; and

- (ab) the nucleotide sequence of the cDNA insert of clone CQ331\_2 deposited with the ATCC under accession number 98278;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
- 10 consisting of:
- (ba) SEQ ID NO:146, but excluding the poly(A) tail at the 3' end of SEQ ID NO:146; and
- (bb) the nucleotide sequence of the cDNA insert of clone CQ331\_2 deposited with the ATCC under accession number 98278;
- 15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- Preferably the polynucleotide isolated according to the above process comprises a nucleotide
- 20 sequence corresponding to the cDNA sequence of SEQ ID NO:146, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:146 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:146, but excluding the poly(A) tail at the 3' end of SEQ ID NO:146. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:146
- 25 from nucleotide 117 to nucleotide 923, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:146 from nucleotide 117 to nucleotide 923, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:146 from nucleotide 117 to nucleotide 923. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ
- 30 ID NO:146 from nucleotide 174 to nucleotide 923, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:146 from nucleotide 174 to nucleotide 923, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:146 from nucleotide 174 to nucleotide 923. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA
- 35 sequence of SEQ ID NO:146 from nucleotide 1 to nucleotide 316, and extending contiguously

from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:146 from nucleotide 1 to nucleotide 316, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:146 from nucleotide 1 to nucleotide 316.

In other embodiments, the present invention provides a composition comprising a protein,  
5 wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:147;
- (b) the amino acid sequence of SEQ ID NO:147 from amino acid 1 to amino acid 57;
- (c) a fragment of the amino acid sequence of SEQ ID NO:147, the fragment  
10 comprising eight contiguous amino acids of SEQ ID NO:147; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CQ331\_2 deposited with the ATCC under accession number 98278;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:147 or the amino acid sequence of SEQ ID  
15 NO:147 from amino acid 1 to amino acid 57. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:147 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:147, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:147 having biological activity,  
20 the fragment comprising the amino acid sequence from amino acid 129 to amino acid 138 of SEQ ID NO:147.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:148;
- 25 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:148 from nucleotide 223 to nucleotide 483;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:148 from nucleotide 22 to nucleotide 397;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length  
30 protein coding sequence of clone CT550\_1 deposited with the ATCC under accession number 98278;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CT550\_1 deposited with the ATCC under accession number 98278;

- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CT550\_1 deposited with the ATCC under accession number 98278;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CT550\_1 deposited with the ATCC under accession number 98278;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:149;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:149 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:149;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:148.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:148 from nucleotide 223 to nucleotide 483; the nucleotide sequence of SEQ ID NO:148 from nucleotide 22 to nucleotide 397; the nucleotide sequence of the full-length protein coding sequence of clone CT550\_1 deposited with the ATCC under accession number 98278; or the nucleotide sequence of a mature protein coding sequence of clone CT550\_1 deposited with the ATCC under accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CT550\_1 deposited with the ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:149 from amino acid 1 to amino acid 58. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:149 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:149, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:149 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:149.



Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:148.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 10 (aa) SEQ ID NO:148, but excluding the poly(A) tail at the 3' end of SEQ ID NO:148; and
- (ab) the nucleotide sequence of the cDNA insert of clone CT550\_1 deposited with the ATCC under accession number 98278;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 15 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
- 20 consisting of:
- (ba) SEQ ID NO:148, but excluding the poly(A) tail at the 3' end of SEQ ID NO:148; and
- (bb) the nucleotide sequence of the cDNA insert of clone CT550\_1 deposited with the ATCC under accession number 98278;
- 25 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide

30 sequence corresponding to the cDNA sequence of SEQ ID NO:148, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:148 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:148, but excluding the poly(A) tail at the 3' end of SEQ ID NO:148. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:148

35 from nucleotide 223 to nucleotide 483, and extending contiguously from a nucleotide sequence

corresponding to the 5' end of said sequence of SEQ ID NO:148 from nucleotide 223 to nucleotide 483, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:148 from nucleotide 223 to nucleotide 483. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ  
5 ID NO:148 from nucleotide 22 to nucleotide 397, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:148 from nucleotide 22 to nucleotide 397, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:148 from nucleotide 22 to nucleotide 397.

In other embodiments, the present invention provides a composition comprising a protein,  
10 wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:149;
- (b) the amino acid sequence of SEQ ID NO:149 from amino acid 1 to amino acid 58;
- (c) a fragment of the amino acid sequence of SEQ ID NO:149, the fragment  
15 comprising eight contiguous amino acids of SEQ ID NO:149; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CT550\_1 deposited with the ATCC under accession number 98278;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:149 or the amino acid sequence of SEQ ID  
20 NO:149 from amino acid 1 to amino acid 58. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:149 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:149, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:149 having biological activity,  
25 the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:149.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:150;
- 30 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:150 from nucleotide 112 to nucleotide 969;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:150 from nucleotide 154 to nucleotide 969;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:150  
35 from nucleotide 1 to nucleotide 423;

- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CT585\_1 deposited with the ATCC under accession number 98278;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CT585\_1 deposited with the ATCC under accession number 98278;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CT585\_1 deposited with the ATCC under accession number 98278;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CT585\_1 deposited with the ATCC under accession number 98278;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:151;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:151 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:151;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:150.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:150 from nucleotide 112 to nucleotide 969; the nucleotide sequence of SEQ ID NO:150 from nucleotide 154 to nucleotide 969; the nucleotide sequence of SEQ ID NO:150 from nucleotide 1 to nucleotide 423; the nucleotide sequence of the full-length protein coding sequence of clone CT585\_1 deposited with the ATCC under accession number 98278; or the nucleotide sequence of a mature protein coding sequence of clone CT585\_1 deposited with the ATCC under accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CT585\_1 deposited with the ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:151 from amino acid 1 to amino acid 104. In further preferred embodiments, the present invention provides

a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:151 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:151, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:151 having biological activity, the fragment comprising the amino acid sequence from amino acid 138 to amino acid 147 of SEQ ID NO:151.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:150.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (aa) SEQ ID NO:150, but excluding the poly(A) tail at the 3' end of SEQ ID NO:150; and

- (ab) the nucleotide sequence of the cDNA insert of clone CT585\_1 deposited with the ATCC under accession number 98278;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

- (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (ba) SEQ ID NO:150, but excluding the poly(A) tail at the 3' end of SEQ ID NO:150; and

- (bb) the nucleotide sequence of the cDNA insert of clone CT585\_1 deposited with the ATCC under accession number 98278;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and

- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:150, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:150 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:150, but excluding the poly(A) tail at the 3' end of SEQ ID NO:150. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:150 from nucleotide 112 to nucleotide 969, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:150 from nucleotide 112 to nucleotide 969, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:150 from nucleotide 112 to nucleotide 969. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:150 from nucleotide 154 to nucleotide 969, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:150 from nucleotide 154 to nucleotide 969, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:150 from nucleotide 154 to nucleotide 969. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:150 from nucleotide 1 to nucleotide 423, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:150 from nucleotide 1 to nucleotide 423, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:150 from nucleotide 1 to nucleotide 423.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:151;
  - (b) the amino acid sequence of SEQ ID NO:151 from amino acid 1 to amino acid 104;
  - (c) a fragment of the amino acid sequence of SEQ ID NO:151, the fragment comprising eight contiguous amino acids of SEQ ID NO:151; and
  - (d) the amino acid sequence encoded by the cDNA insert of clone CT585\_1 deposited with the ATCC under accession number 98278;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:151 or the amino acid sequence of SEQ ID NO:151 from amino acid 1 to amino acid 104. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:151 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:151, or a protein

comprising a fragment of the amino acid sequence of SEQ ID NO:151 having biological activity, the fragment comprising the amino acid sequence from amino acid 138 to amino acid 147 of SEQ ID NO:151.

In one embodiment, the present invention provides a composition comprising an isolated  
5 polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:152;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:152  
from nucleotide 37 to nucleotide 2766;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:152  
10 from nucleotide 243 to nucleotide 789;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length  
protein coding sequence of clone CT797\_3 deposited with the ATCC under accession  
number 98278;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA  
15 insert of clone CT797\_3 deposited with the ATCC under accession number 98278;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein  
coding sequence of clone CT797\_3 deposited with the ATCC under accession number  
98278;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert  
20 of clone CT797\_3 deposited with the ATCC under accession number 98278;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence  
of SEQ ID NO:153;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino  
acid sequence of SEQ ID NO:153 having biological activity, the fragment comprising  
25 eight contiguous amino acids of SEQ ID NO:153;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g)  
above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h)  
or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of  
30 the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of  
the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the  
length of SEQ ID NO:152.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:152 from nucleotide 37 to nucleotide 2766; the nucleotide sequence of SEQ ID NO:152 from nucleotide 243 to nucleotide 789; the nucleotide sequence of the full-length protein coding sequence of clone CT797\_3 deposited with the ATCC under accession number 98278; or the  
5 nucleotide sequence of a mature protein coding sequence of clone CT797\_3 deposited with the ATCC under accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CT797\_3 deposited with the ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid  
10 sequence of SEQ ID NO:153 from amino acid 75 to amino acid 251. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:153 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:153, or a polynucleotide encoding a protein comprising a fragment of the  
15 amino acid sequence of SEQ ID NO:153 having biological activity, the fragment comprising the amino acid sequence from amino acid 450 to amino acid 459 of SEQ ID NO:153.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:152.

Further embodiments of the invention provide isolated polynucleotides produced  
20 according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
    - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
      - 25 (aa) SEQ ID NO:152, but excluding the poly(A) tail at the 3' end of SEQ ID NO:152; and
      - (ab) the nucleotide sequence of the cDNA insert of clone CT797\_3 deposited with the ATCC under accession number 98278;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions  
30 at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

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(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:152, but excluding the poly(A) tail at the 3' end of SEQ ID NO:152; and

(bb) the nucleotide sequence of the cDNA insert of clone CT797\_3 deposited with the ATCC under accession number 98278;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

10 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:152, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:152 to a nucleotide  
15 sequence corresponding to the 3' end of SEQ ID NO:152, but excluding the poly(A) tail at the 3' end of SEQ ID NO:152. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:152 from nucleotide 37 to nucleotide 2766, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:152 from nucleotide 37 to nucleotide  
20 2766, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:152 from nucleotide 37 to nucleotide 2766. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:152 from nucleotide 243 to nucleotide 789, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:152 from nucleotide 243  
25 to nucleotide 789, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:152 from nucleotide 243 to nucleotide 789.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:153;  
30 (b) the amino acid sequence of SEQ ID NO:153 from amino acid 75 to amino acid 251;

(c) a fragment of the amino acid sequence of SEQ ID NO:153, the fragment comprising eight contiguous amino acids of SEQ ID NO:153; and

(d) the amino acid sequence encoded by the cDNA insert of clone CT797\_3  
35 deposited with the ATCC under accession number 98278;



the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:153 or the amino acid sequence of SEQ ID NO:153 from amino acid 75 to amino acid 251. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:153 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:153, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:153 having biological activity, the fragment comprising the amino acid sequence from amino acid 450 to amino acid 459 of SEQ ID NO:153.

10 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:155;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:155 from nucleotide 41 to nucleotide 760;
- 15 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CB107\_1 deposited with the ATCC under accession number 98279;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CB107\_1 deposited with the ATCC under accession number 98279;
- 20 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CB107\_1 deposited with the ATCC under accession number 98279;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CB107\_1 deposited with the ATCC under accession number 98279;
- 25 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:156;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:156;
- 30 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of
- 35 the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:155.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:155  
5 from nucleotide 41 to nucleotide 760; the nucleotide sequence of the full-length protein coding sequence of clone CB107\_1 deposited with the ATCC under accession number 98279; or the nucleotide sequence of a mature protein coding sequence of clone CB107\_1 deposited with the ATCC under accession number 98279. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CB107\_1  
10 deposited with the ATCC under accession number 98279. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:156 from amino acid 127 to amino acid 240. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment  
15 preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:156, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment comprising the amino acid sequence from amino acid 115 to amino acid 124 of SEQ ID NO:156.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID  
20 NO:155, SEQ ID NO:154, and SEQ ID NO:157.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X  
25 SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:154;
    - (ab) SEQ ID NO:155;
    - (ac) SEQ ID NO:157, but excluding the poly(A) tail at the 3'  
30 end of SEQ ID NO:157; and
    - (ad) the nucleotide sequence of the cDNA insert of clone CB107\_1 deposited with the ATCC under accession number 98279;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - 35 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:154;

(bb) SEQ ID NO:155;

(bc) SEQ ID NO:157, but excluding the poly(A) tail at the 3' end of SEQ ID NO:157; and

(bd) the nucleotide sequence of the cDNA insert of clone CB107\_1 deposited with the ATCC under accession number 98279;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:154, SEQ ID NO:155, and SEQ ID NO:157, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:154 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:157, but excluding the poly(A) tail at the 3' end of SEQ ID NO:157. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:155, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:155 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:155. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:155 from nucleotide 41 to nucleotide 760, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:155 from nucleotide 41 to nucleotide 760, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:155 from nucleotide 41 to nucleotide 760.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:156;

(b) the amino acid sequence of SEQ ID NO:156 from amino acid 127 to amino acid 240;

- (c) a fragment of the amino acid sequence of SEQ ID NO:156, the fragment comprising eight contiguous amino acids of SEQ ID NO:156; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CB107\_1 deposited with the ATCC under accession number 98279;
- 5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:156 or the amino acid sequence of SEQ ID NO:156 from amino acid 127 to amino acid 240. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment preferably comprising eight (more preferably
- 10 twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:156, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment comprising the amino acid sequence from amino acid 115 to amino acid 124 of SEQ ID NO:156.

In one embodiment, the present invention provides a composition comprising an isolated

15 polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:158;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:158 from nucleotide 374 to nucleotide 1108;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:158
- 20 from nucleotide 500 to nucleotide 1108;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:158 from nucleotide 1 to nucleotide 387;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CG300\_3 deposited with the ATCC under accession
- 25 number 98279;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CG300\_3 deposited with the ATCC under accession number 98279;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CG300\_3 deposited with the ATCC under accession number
- 30 98279;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CG300\_3 deposited with the ATCC under accession number 98279;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:159;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:159 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:159;

5 (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

10 (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:158.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:158 from nucleotide 374 to nucleotide 1108; the nucleotide sequence of SEQ ID NO:158 from  
15 nucleotide 500 to nucleotide 1108; the nucleotide sequence of SEQ ID NO:158 from nucleotide 1 to nucleotide 387; the nucleotide sequence of the full-length protein coding sequence of clone CG300\_3 deposited with the ATCC under accession number 98279; or the nucleotide sequence of a mature protein coding sequence of clone CG300\_3 deposited with the ATCC under accession number 98279. In other preferred embodiments, the polynucleotide encodes the full-length or a  
20 mature protein encoded by the cDNA insert of clone CG300\_3 deposited with the ATCC under accession number 98279. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:159 from amino acid 23 to amino acid 57. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ  
25 ID NO:159 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:159, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:159 having biological activity, the fragment comprising the amino acid sequence from amino acid 117 to amino acid 126 of SEQ ID NO:159.

30 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:158.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

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(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5

(aa) SEQ ID NO:158, but excluding the poly(A) tail at the 3' end of SEQ ID NO:158; and

(ab) the nucleotide sequence of the cDNA insert of clone CG300\_3 deposited with the ATCC under accession number 98279;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

10

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:158, but excluding the poly(A) tail at the 3' end of SEQ ID NO:158; and

(bb) the nucleotide sequence of the cDNA insert of clone CG300\_3 deposited with the ATCC under accession number 98279;

20

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide  
25 sequence corresponding to the cDNA sequence of SEQ ID NO:158, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:158 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:158, but excluding the poly(A) tail at the 3' end of SEQ ID NO:158. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:158  
30 from nucleotide 374 to nucleotide 1108, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:158 from nucleotide 374 to nucleotide 1108, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:158 from nucleotide 374 to nucleotide 1108. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of  
35 SEQ ID NO:158 from nucleotide 500 to nucleotide 1108, and extending contiguously from a

nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:158 from nucleotide 500 to nucleotide 1108, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:158 from nucleotide 500 to nucleotide 1108. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence  
5 corresponding to the cDNA sequence of SEQ ID NO:158 from nucleotide 1 to nucleotide 387, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:158 from nucleotide 1 to nucleotide 387, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:158 from nucleotide 1 to nucleotide 387.

In other embodiments, the present invention provides a composition comprising a protein,  
10 wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:159;
- (b) the amino acid sequence of SEQ ID NO:159 from amino acid 23 to amino acid 57;
- (c) a fragment of the amino acid sequence of SEQ ID NO:159, the fragment  
15 comprising eight contiguous amino acids of SEQ ID NO:159; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CG300\_3 deposited with the ATCC under accession number 98279;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:159 or the amino acid sequence of SEQ ID  
20 NO:159 from amino acid 23 to amino acid 57. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:159 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:159, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:159 having biological activity,  
25 the fragment comprising the amino acid sequence from amino acid 117 to amino acid 126 of SEQ ID NO:159.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:160;
- 30 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:160 from nucleotide 126 to nucleotide 3053;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:160 from nucleotide 180 to nucleotide 3053;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:160  
35 from nucleotide 49 to nucleotide 382;

- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CJ145\_1 deposited with the ATCC under accession number 98279;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CJ145\_1 deposited with the ATCC under accession number 98279;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CJ145\_1 deposited with the ATCC under accession number 98279;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CJ145\_1 deposited with the ATCC under accession number 98279;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:161;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:161 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:161;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:160.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:160 from nucleotide 126 to nucleotide 3053; the nucleotide sequence of SEQ ID NO:160 from nucleotide 180 to nucleotide 3053; the nucleotide sequence of SEQ ID NO:160 from nucleotide 49 to nucleotide 382; the nucleotide sequence of the full-length protein coding sequence of clone CJ145\_1 deposited with the ATCC under accession number 98279; or the nucleotide sequence of a mature protein coding sequence of clone CJ145\_1 deposited with the ATCC under accession number 98279. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CJ145\_1 deposited with the ATCC under accession number 98279. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:161 from amino acid 1 to amino acid 87. In further preferred embodiments, the present invention provides



a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:161 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:161, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:161 having  
5 biological activity, the fragment comprising the amino acid sequence from amino acid 482 to amino acid 491 of SEQ ID NO:161.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:160.

Further embodiments of the invention provide isolated polynucleotides produced  
10 according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

15 (aa) SEQ ID NO:160, but excluding the poly(A) tail at the 3' end of SEQ ID NO:160; and

(ab) the nucleotide sequence of the cDNA insert of clone CJ145\_1 deposited with the ATCC under accession number 98279;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:

25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:160, but excluding the poly(A) tail at the 3' end of SEQ ID NO:160; and

30 (bb) the nucleotide sequence of the cDNA insert of clone CJ145\_1 deposited with the ATCC under accession number 98279;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:160, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:160 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:160, but excluding the poly(A) tail at the 3' end of SEQ ID NO:160. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:160 from nucleotide 126 to nucleotide 3053, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:160 from nucleotide 126 to nucleotide 3053, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:160 from nucleotide 126 to nucleotide 3053. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:160 from nucleotide 180 to nucleotide 3053, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:160 from nucleotide 180 to nucleotide 3053, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:160 from nucleotide 180 to nucleotide 3053. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:160 from nucleotide 49 to nucleotide 382, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:160 from nucleotide 49 to nucleotide 382, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:160 from nucleotide 49 to nucleotide 382.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:161;
- (b) the amino acid sequence of SEQ ID NO:161 from amino acid 1 to amino acid 87;
- (c) a fragment of the amino acid sequence of SEQ ID NO:161, the fragment comprising eight contiguous amino acids of SEQ ID NO:161; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CJ145\_1 deposited with the ATCC under accession number 98279;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:161 or the amino acid sequence of SEQ ID NO:161 from amino acid 1 to amino acid 87. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:161 having biological activity, the fragment preferably comprising eight (more preferably

twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:161, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:161 having biological activity, the fragment comprising the amino acid sequence from amino acid 482 to amino acid 491 of SEQ ID NO:161.

5           In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:162;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:162 from nucleotide 40 to nucleotide 342;
- 10           (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:162 from nucleotide 127 to nucleotide 342;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:162 from nucleotide 11 to nucleotide 181;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length  
15           protein coding sequence of clone CJ160\_11 deposited with the ATCC under accession number 98279;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CJ160\_11 deposited with the ATCC under accession number 98279;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein  
20           coding sequence of clone CJ160\_11 deposited with the ATCC under accession number 98279;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CJ160\_11 deposited with the ATCC under accession number 98279;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence  
25           of SEQ ID NO:163;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:163 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:163;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h)  
30           above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:162.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:162  
5 from nucleotide 40 to nucleotide 342; the nucleotide sequence of SEQ ID NO:162 from nucleotide 127 to nucleotide 342; the nucleotide sequence of SEQ ID NO:162 from nucleotide 11 to nucleotide 181; the nucleotide sequence of the full-length protein coding sequence of clone CJ160\_11 deposited with the ATCC under accession number 98279; or the nucleotide sequence of a mature protein coding sequence of clone CJ160\_11 deposited with the ATCC under accession  
10 number 98279. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CJ160\_11 deposited with the ATCC under accession number 98279. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:163 from amino acid 7 to amino acid 48. In further preferred embodiments, the present invention provides  
15 a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:163 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:163, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:163 having biological activity, the fragment comprising the amino acid sequence from amino acid 45 to amino  
20 acid 54 of SEQ ID NO:163.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:162.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 25 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 30 (aa) SEQ ID NO:162, but excluding the poly(A) tail at the 3' end of SEQ ID NO:162; and
- (ab) the nucleotide sequence of the cDNA insert of clone CJ160\_11 deposited with the ATCC under accession number 98279;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 35 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:162, but excluding the poly(A) tail at the 3' end of SEQ ID NO:162; and

(bb) the nucleotide sequence of the cDNA insert of clone CJ160\_11 deposited with the ATCC under accession number 98279;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:162, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:162 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:162, but excluding the poly(A) tail at the 3' end of SEQ ID NO:162. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:162 from nucleotide 40 to nucleotide 342, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:162 from nucleotide 40 to nucleotide 342, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:162 from nucleotide 40 to nucleotide 342. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:162 from nucleotide 127 to nucleotide 342, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:162 from nucleotide 127 to nucleotide 342, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:162 from nucleotide 127 to nucleotide 342. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:162 from nucleotide 11 to nucleotide 181, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:162 from nucleotide 11 to nucleotide 181, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:162 from nucleotide 11 to nucleotide 181.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:163;
  - (b) the amino acid sequence of SEQ ID NO:163 from amino acid 7 to amino acid 48;
  - (c) a fragment of the amino acid sequence of SEQ ID NO:163, the fragment comprising eight contiguous amino acids of SEQ ID NO:163; and
  - (d) the amino acid sequence encoded by the cDNA insert of clone CJ160\_11 deposited with the ATCC under accession number 98279;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:163 or the amino acid sequence of SEQ ID NO:163 from amino acid 7 to amino acid 48. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:163 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:163, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:163 having biological activity, the fragment comprising the amino acid sequence from amino acid 45 to amino acid 54 of SEQ ID NO:163.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:164;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:164 from nucleotide 180 to nucleotide 467;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:164 from nucleotide 267 to nucleotide 467;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CO20\_1 deposited with the ATCC under accession number 98279;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CO20\_1 deposited with the ATCC under accession number 98279;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CO20\_1 deposited with the ATCC under accession number 98279;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CO20\_1 deposited with the ATCC under accession number 98279;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:165;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:165 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:165;

5 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

10 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:164.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:164 from nucleotide 180 to nucleotide 467; the nucleotide sequence of SEQ ID NO:164 from  
15 nucleotide 267 to nucleotide 467; the nucleotide sequence of the full-length protein coding sequence of clone CO20\_1 deposited with the ATCC under accession number 98279; or the nucleotide sequence of a mature protein coding sequence of clone CO20\_1 deposited with the ATCC under accession number 98279. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CO20\_1  
20 deposited with the ATCC under accession number 98279. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:165 from amino acid 1 to amino acid 37. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:165 having biological activity, the fragment  
25 preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:165, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:165 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:165.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID  
30 NO:164 and SEQ ID NO:166.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:164;

5 (ab) SEQ ID NO:166, but excluding the poly(A) tail at the 3' end of SEQ ID NO:166; and

(ac) the nucleotide sequence of the cDNA insert of clone CO20\_1 deposited with the ATCC under accession number 98279;

10 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:164;

(bb) SEQ ID NO:166, but excluding the poly(A) tail at the 3' end of SEQ ID NO:166; and

20 (bc) the nucleotide sequence of the cDNA insert of clone CO20\_1 deposited with the ATCC under accession number 98279;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

25 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:164 and SEQ ID NO:166, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:164 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:166, but excluding the poly(A) tail at the 3' end of SEQ ID NO:166. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:164, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:164 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:164. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:164

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from nucleotide 180 to nucleotide 467, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:164 from nucleotide 180 to nucleotide 467, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:164 from nucleotide 180 to nucleotide 467. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:164 from nucleotide 267 to nucleotide 467, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:164 from nucleotide 267 to nucleotide 467, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:164 from nucleotide 267 to nucleotide 467.

10 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:165;
- (b) the amino acid sequence of SEQ ID NO:165 from amino acid 1 to amino acid 37;
- 15 (c) a fragment of the amino acid sequence of SEQ ID NO:165, the fragment comprising eight contiguous amino acids of SEQ ID NO:165; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CO20\_1 deposited with the ATCC under accession number 98279;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:165 or the amino acid sequence of SEQ ID NO:165 from amino acid 1 to amino acid 37. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:165 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:165, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:165 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:165.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:167;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:167 from nucleotide 176 to nucleotide 520;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:167 from nucleotide 317 to nucleotide 520;

- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:167 from nucleotide 118 to nucleotide 413;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CO223\_3 deposited with the ATCC under accession number 98291;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CO223\_3 deposited with the ATCC under accession number 98291;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CO223\_3 deposited with the ATCC under accession number 98291;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CO223\_3 deposited with the ATCC under accession number 98291;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:168;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:168 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:168;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:167.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:167 from nucleotide 176 to nucleotide 520; the nucleotide sequence of SEQ ID NO:167 from nucleotide 317 to nucleotide 520; the nucleotide sequence of SEQ ID NO:167 from nucleotide 118 to nucleotide 413; the nucleotide sequence of the full-length protein coding sequence of clone CO223\_3 deposited with the ATCC under accession number 98291; or the nucleotide sequence of a mature protein coding sequence of clone CO223\_3 deposited with the ATCC under accession number 98291. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CO223\_3 deposited with the ATCC under accession number 98291. In yet other preferred embodiments, the present invention provides a

polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:168 from amino acid 1 to amino acid 80. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:168 having biological activity, the fragment preferably comprising eight (more preferably  
5 twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:168, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:168 having biological activity, the fragment comprising the amino acid sequence from amino acid 52 to amino acid 61 of SEQ ID NO:168.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID  
10 NO:167.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X  
15 SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:167, but excluding the poly(A) tail at the 3' end of SEQ ID NO:167; and
    - (ab) the nucleotide sequence of the cDNA insert of clone  
20 CO223\_3 deposited with the ATCC under accession number 98291;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- 25 (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:167, but excluding the poly(A) tail at the 3'  
30 end of SEQ ID NO:167; and
    - (bb) the nucleotide sequence of the cDNA insert of clone CO223\_3 deposited with the ATCC under accession number 98291;
    - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
    - 35 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:167, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:167 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:167, but excluding the poly(A) tail at the 3' end of SEQ ID NO:167. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:167 from nucleotide 176 to nucleotide 520, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:167 from nucleotide 176 to nucleotide 520, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:167 from nucleotide 176 to nucleotide 520. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:167 from nucleotide 317 to nucleotide 520, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:167 from nucleotide 317 to nucleotide 520, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:167 from nucleotide 317 to nucleotide 520. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:167 from nucleotide 118 to nucleotide 413, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:167 from nucleotide 118 to nucleotide 413, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:167 from nucleotide 118 to nucleotide 413.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:168;
- (b) the amino acid sequence of SEQ ID NO:168 from amino acid 1 to amino acid 80;
- (c) a fragment of the amino acid sequence of SEQ ID NO:168, the fragment comprising eight contiguous amino acids of SEQ ID NO:168; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CO223\_3 deposited with the ATCC under accession number 98291;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:168 or the amino acid sequence of SEQ ID NO:168 from amino acid 1 to amino acid 80. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:168 having biological activity, the fragment preferably comprising eight (more preferably

twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:168, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:168 having biological activity, the fragment comprising the amino acid sequence from amino acid 52 to amino acid 61 of SEQ ID NO:168.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:169;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:169 from nucleotide 303 to nucleotide 542;
- 10 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:169 from nucleotide 1 to nucleotide 435;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CO310\_2 deposited with the ATCC under accession number 98279;
- 15 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CO310\_2 deposited with the ATCC under accession number 98279;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CO310\_2 deposited with the ATCC under accession number 98279;
- 20 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CO310\_2 deposited with the ATCC under accession number 98279;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:170;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:170 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:170;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:169.
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Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:169 from nucleotide 303 to nucleotide 542; the nucleotide sequence of SEQ ID NO:169 from nucleotide 1 to nucleotide 435; the nucleotide sequence of the full-length protein coding sequence of clone CO310\_2 deposited with the ATCC under accession number 98279; or the nucleotide  
5 sequence of a mature protein coding sequence of clone CO310\_2 deposited with the ATCC under accession number 98279. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CO310\_2 deposited with the ATCC under accession number 98279. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID  
10 NO:170 from amino acid 1 to amino acid 44. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:170 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:170, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ  
15 ID NO:170 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:170.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:169.

Further embodiments of the invention provide isolated polynucleotides produced  
20 according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - 25 (aa) SEQ ID NO:169, but excluding the poly(A) tail at the 3' end of SEQ ID NO:169; and
    - (ab) the nucleotide sequence of the cDNA insert of clone CO310\_2 deposited with the ATCC under accession number 98279;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions  
30 at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:169, but excluding the poly(A) tail at the 3' end of SEQ ID NO:169; and

(bb) the nucleotide sequence of the cDNA insert of clone CO310\_2 deposited with the ATCC under accession number 98279;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

10 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:169, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:169 to a nucleotide  
15 sequence corresponding to the 3' end of SEQ ID NO:169, but excluding the poly(A) tail at the 3' end of SEQ ID NO:169. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:169 from nucleotide 303 to nucleotide 542, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:169 from nucleotide 303 to nucleotide  
20 542, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:169 from nucleotide 303 to nucleotide 542. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:169 from nucleotide 1 to nucleotide 435, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:169 from nucleotide 1 to  
25 nucleotide 435, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:169 from nucleotide 1 to nucleotide 435.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 30 (a) the amino acid sequence of SEQ ID NO:170;
- (b) the amino acid sequence of SEQ ID NO:170 from amino acid 1 to amino acid 44;
- (c) a fragment of the amino acid sequence of SEQ ID NO:170, the fragment comprising eight contiguous amino acids of SEQ ID NO:170; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CO310\_2  
35 deposited with the ATCC under accession number 98279;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:170 or the amino acid sequence of SEQ ID NO:170 from amino acid 1 to amino acid 44. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID  
5 NO:170 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:170, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:170 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:170.

10 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:171;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:171 from nucleotide 40 to nucleotide 455;
- 15 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:171 from nucleotide 85 to nucleotide 455;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:171 from nucleotide 265 to nucleotide 515;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CP258\_3 deposited with the ATCC under accession number 98279;
- 20 (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CP258\_3 deposited with the ATCC under accession number 98279;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CP258\_3 deposited with the ATCC under accession number 98279;
- 25 (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CP258\_3 deposited with the ATCC under accession number 98279;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:172;
- 30 (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:172 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:172;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h)
- 35 above;



(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

5 (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:171.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:171 from nucleotide 40 to nucleotide 455; the nucleotide sequence of SEQ ID NO:171 from nucleotide  
10 85 to nucleotide 455; the nucleotide sequence of SEQ ID NO:171 from nucleotide 265 to nucleotide 515; the nucleotide sequence of the full-length protein coding sequence of clone CP258\_3 deposited with the ATCC under accession number 98279; or the nucleotide sequence of a mature protein coding sequence of clone CP258\_3 deposited with the ATCC under accession number 98279. In other preferred embodiments, the polynucleotide encodes the full-length or a  
15 mature protein encoded by the cDNA insert of clone CP258\_3 deposited with the ATCC under accession number 98279. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:172 from amino acid 64 to amino acid 138. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence  
20 of SEQ ID NO:172 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:172, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:172 having biological activity, the fragment comprising the amino acid sequence from amino acid 64 to amino acid 73 of SEQ ID NO:172.

25 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:171.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:171, but excluding the poly(A) tail at the 3' end of SEQ ID NO:171; and

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- (ab) the nucleotide sequence of the cDNA insert of clone CP258\_3 deposited with the ATCC under accession number 98279;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
- 10 consisting of:
- (ba) SEQ ID NO:171, but excluding the poly(A) tail at the 3' end of SEQ ID NO:171; and
- (bb) the nucleotide sequence of the cDNA insert of clone CP258\_3 deposited with the ATCC under accession number 98279;
- 15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).
- Preferably the polynucleotide isolated according to the above process comprises a nucleotide
- 20 sequence corresponding to the cDNA sequence of SEQ ID NO:171, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:171 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:171, but excluding the poly(A) tail at the 3' end of SEQ ID NO:171. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:171
- 25 from nucleotide 40 to nucleotide 455, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:171 from nucleotide 40 to nucleotide 455, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:171 from nucleotide 40 to nucleotide 455. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ
- 30 ID NO:171 from nucleotide 85 to nucleotide 455, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:171 from nucleotide 85 to nucleotide 455, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:171 from nucleotide 85 to nucleotide 455. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA
- 35 sequence of SEQ ID NO:171 from nucleotide 265 to nucleotide 515, and extending contiguously

from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:171 from nucleotide 265 to nucleotide 515, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:171 from nucleotide 265 to nucleotide 515.

- In other embodiments, the present invention provides a composition comprising a protein,
- 5 wherein said protein comprises an amino acid sequence selected from the group consisting of:
- (a) the amino acid sequence of SEQ ID NO:172;
  - (b) the amino acid sequence of SEQ ID NO:172 from amino acid 64 to amino acid 138;
  - (c) a fragment of the amino acid sequence of SEQ ID NO:172, the fragment
  - 10 comprising eight contiguous amino acids of SEQ ID NO:172; and
  - (d) the amino acid sequence encoded by the cDNA insert of clone CP258\_3 deposited with the ATCC under accession number 98279;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:172 or the amino acid sequence of SEQ ID

15 NO:172 from amino acid 64 to amino acid 138. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:172 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:172, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:172 having biological activity,

20 the fragment comprising the amino acid sequence from amino acid 64 to amino acid 73 of SEQ ID NO:172.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:173;
- 25 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:173 from nucleotide 105 to nucleotide 1007;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:173 from nucleotide 801 to nucleotide 1007;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:173
- 30 from nucleotide 1 to nucleotide 352;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CW1155\_3 deposited with the ATCC under accession number 98279;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA
- 35 insert of clone CW1155\_3 deposited with the ATCC under accession number 98279;

- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CW1155\_3 deposited with the ATCC under accession number 98279;
- 5 (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CW1155\_3 deposited with the ATCC under accession number 98279;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:174;
- 10 (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:174 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:174;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- 15 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:173.
- 20 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:173 from nucleotide 105 to nucleotide 1007; the nucleotide sequence of SEQ ID NO:173 from nucleotide 801 to nucleotide 1007; the nucleotide sequence of SEQ ID NO:173 from nucleotide 1 to nucleotide 352; the nucleotide sequence of the full-length protein coding sequence of clone CW1155\_3 deposited with the ATCC under accession number 98279; or the nucleotide sequence
- 25 of a mature protein coding sequence of clone CW1155\_3 deposited with the ATCC under accession number 98279. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CW1155\_3 deposited with the ATCC under accession number 98279. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID
- 30 NO:174 from amino acid 1 to amino acid 83. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:174 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:174, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:174 having biological activity, the fragment comprising the amino acid sequence from amino acid 145 to amino acid 154 of SEQ ID NO:174.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:173.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:173, but excluding the poly(A) tail at the 3' end of SEQ ID NO:173; and

(ab) the nucleotide sequence of the cDNA insert of clone CW1155\_3 deposited with the ATCC under accession number 98279;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

20 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:173, but excluding the poly(A) tail at the 3' end of SEQ ID NO:173; and

25 (bb) the nucleotide sequence of the cDNA insert of clone CW1155\_3 deposited with the ATCC under accession number 98279;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

30 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:173, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:173 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:173, but excluding the poly(A) tail at the 3' end of SEQ ID NO:173. Also preferably the polynucleotide isolated according to the above

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process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:173 from nucleotide 105 to nucleotide 1007, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:173 from nucleotide 105 to nucleotide 1007, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:173 from nucleotide 105 to nucleotide 1007. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:173 from nucleotide 801 to nucleotide 1007, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:173 from nucleotide 801 to nucleotide 1007, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:173 from nucleotide 801 to nucleotide 1007. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:173 from nucleotide 1 to nucleotide 352, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:173 from nucleotide 1 to nucleotide 352, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:173 from nucleotide 1 to nucleotide 352.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:174;
  - (b) the amino acid sequence of SEQ ID NO:174 from amino acid 1 to amino acid 83;
  - (c) a fragment of the amino acid sequence of SEQ ID NO:174, the fragment comprising eight contiguous amino acids of SEQ ID NO:174; and
  - (d) the amino acid sequence encoded by the cDNA insert of clone CW1155\_3 deposited with the ATCC under accession number 98279;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:174 or the amino acid sequence of SEQ ID NO:174 from amino acid 1 to amino acid 83. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:174 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:174, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:174 having biological activity, the fragment comprising the amino acid sequence from amino acid 145 to amino acid 154 of SEQ ID NO:174.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:175;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:175 from nucleotide 11 to nucleotide 1699;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:175 from nucleotide 1682 to nucleotide 1699;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:175 from nucleotide 737 to nucleotide 1134;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CZ247\_2 deposited with the ATCC under accession number 98279;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CZ247\_2 deposited with the ATCC under accession number 98279;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CZ247\_2 deposited with the ATCC under accession number 98279;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CZ247\_2 deposited with the ATCC under accession number 98279;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:176;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:176 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:176;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:175.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:175 from nucleotide 11 to nucleotide 1699; the nucleotide sequence of SEQ ID NO:175 from nucleotide 1682 to nucleotide 1699; the nucleotide sequence of SEQ ID NO:175 from nucleotide 737 to nucleotide 1134; the nucleotide sequence of the full-length protein coding sequence of

clone CZ247\_2 deposited with the ATCC under accession number 98279; or the nucleotide sequence of a mature protein coding sequence of clone CZ247\_2 deposited with the ATCC under accession number 98279. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CZ247\_2 deposited with the  
5 ATCC under accession number 98279. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:176 from amino acid 298 to amino acid 374. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:176 having biological activity, the fragment preferably comprising eight  
10 (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:176, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:176 having biological activity, the fragment comprising the amino acid sequence from amino acid 276 to amino acid 285 of SEQ ID NO:176.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID  
15 NO:175.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:  
(i) preparing one or more polynucleotide probes that hybridize in 6X  
20 SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:175, but excluding the poly(A) tail at the 3' end of SEQ ID NO:175; and  
(ab) the nucleotide sequence of the cDNA insert of clone  
25 CZ247\_2 deposited with the ATCC under accession number 98279;  
(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and  
(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:  
(i) preparing one or more polynucleotide primers that hybridize in  
30 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:  
(ba) SEQ ID NO:175, but excluding the poly(A) tail at the 3'  
35 end of SEQ ID NO:175; and



- (bb) the nucleotide sequence of the cDNA insert of clone CZ247\_2 deposited with the ATCC under accession number 98279;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 5 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:175, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:175 to a nucleotide  
10 sequence corresponding to the 3' end of SEQ ID NO:175, but excluding the poly(A) tail at the 3' end of SEQ ID NO:175. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:175 from nucleotide 11 to nucleotide 1699, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:175 from nucleotide 11 to nucleotide  
15 1699, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:175 from nucleotide 11 to nucleotide 1699. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:175 from nucleotide 1682 to nucleotide 1699, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:175 from  
20 nucleotide 1682 to nucleotide 1699, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:175 from nucleotide 1682 to nucleotide 1699. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:175 from nucleotide 737 to nucleotide 1134, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said  
25 sequence of SEQ ID NO:175 from nucleotide 737 to nucleotide 1134, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:175 from nucleotide 737 to nucleotide 1134.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 30 (a) the amino acid sequence of SEQ ID NO:176;
- (b) the amino acid sequence of SEQ ID NO:176 from amino acid 298 to amino acid 374;
- (c) a fragment of the amino acid sequence of SEQ ID NO:176, the fragment comprising eight contiguous amino acids of SEQ ID NO:176; and

(d) the amino acid sequence encoded by the cDNA insert of clone CZ247\_2 deposited with the ATCC under accession number 98279; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:176 or the amino acid sequence of SEQ ID NO:176 from amino acid 298 to amino acid 374. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:176 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:176, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:176 having biological activity, the fragment comprising the amino acid sequence from amino acid 276 to amino acid 285 of SEQ ID NO:176.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:177;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:177 from nucleotide 918 to nucleotide 1262;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:177 from nucleotide 999 to nucleotide 1262;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:177 from nucleotide 928 to nucleotide 1134;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AM666\_1 deposited with the ATCC under accession number 98292;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AM666\_1 deposited with the ATCC under accession number 98292;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AM666\_1 deposited with the ATCC under accession number 98292;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AM666\_1 deposited with the ATCC under accession number 98292;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:178;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:178 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:178;

- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- 5 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:177.
- 10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:177 from nucleotide 918 to nucleotide 1262; the nucleotide sequence of SEQ ID NO:177 from nucleotide 999 to nucleotide 1262; the nucleotide sequence of SEQ ID NO:177 from nucleotide 928 to nucleotide 1134; the nucleotide sequence of the full-length protein coding sequence of clone AM666\_1 deposited with the ATCC under accession number 98292; or the nucleotide
- 15 sequence of a mature protein coding sequence of clone AM666\_1 deposited with the ATCC under accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AM666\_1 deposited with the ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID
- 20 NO:178 from amino acid 5 to amino acid 72. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:178 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:178, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ
- 25 ID NO:178 having biological activity, the fragment comprising the amino acid sequence from amino acid 52 to amino acid 61 of SEQ ID NO:178.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:177.

Further embodiments of the invention provide isolated polynucleotides produced

30 according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

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(aa) SEQ ID NO:177, but excluding the poly(A) tail at the 3' end of SEQ ID NO:177; and

(ab) the nucleotide sequence of the cDNA insert of clone AM666\_1 deposited with the ATCC under accession number 98292;

5 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

10 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:177, but excluding the poly(A) tail at the 3' end of SEQ ID NO:177; and

15 (bb) the nucleotide sequence of the cDNA insert of clone AM666\_1 deposited with the ATCC under accession number 98292;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

20 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:177, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:177 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:177, but excluding the poly(A) tail at the 3' end of SEQ ID NO:177. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:177 from nucleotide 918 to nucleotide 1262, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:177 from nucleotide 918 to nucleotide 1262, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:177 from nucleotide 918 to nucleotide 1262. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:177 from nucleotide 999 to nucleotide 1262, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:177 from nucleotide 999 to nucleotide 1262, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:177 from nucleotide 999 to nucleotide 1262. Also preferably the

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polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:177 from nucleotide 928 to nucleotide 1134, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:177 from nucleotide 928 to nucleotide 1134, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:177 from nucleotide 928 to nucleotide 1134.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:178;
- 10 (b) the amino acid sequence of SEQ ID NO:178 from amino acid 5 to amino acid 72;
- (c) a fragment of the amino acid sequence of SEQ ID NO:178, the fragment comprising eight contiguous amino acids of SEQ ID NO:178; and
- (d) the amino acid sequence encoded by the cDNA insert of clone AM666\_1
- 15 deposited with the ATCC under accession number 98292;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:178 or the amino acid sequence of SEQ ID NO:178 from amino acid 5 to amino acid 72. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:178 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:178, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:178 having biological activity, the fragment comprising the amino acid sequence from amino acid 52 to amino acid 61 of SEQ ID NO:178.

25 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:179;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:179 from nucleotide 751 to nucleotide 906;
- 30 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:179 from nucleotide 829 to nucleotide 906;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:179 from nucleotide 556 to nucleotide 831;

- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BN387\_3 deposited with the ATCC under accession number 98292;
- 5 (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BN387\_3 deposited with the ATCC under accession number 98292;
- (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BN387\_3 deposited with the ATCC under accession number 98292;
- 10 (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BN387\_3 deposited with the ATCC under accession number 98292;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:180;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:180 having biological activity, the fragment comprising  
15 eight contiguous amino acids of SEQ ID NO:180;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;
- 20 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:179.
- 25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:179 from nucleotide 751 to nucleotide 906; the nucleotide sequence of SEQ ID NO:179 from nucleotide 829 to nucleotide 906; the nucleotide sequence of SEQ ID NO:179 from nucleotide 556 to nucleotide 831; the nucleotide sequence of the full-length protein coding sequence of clone BN387\_3 deposited with the ATCC under accession number 98292; or the nucleotide sequence  
30 of a mature protein coding sequence of clone BN387\_3 deposited with the ATCC under accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BN387\_3 deposited with the ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:180 from  
35 amino acid 1 to amino acid 27. In further preferred embodiments, the present invention provides

a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:180 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:180, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:180 having biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:180.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:179.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (aa) SEQ ID NO:179, but excluding the poly(A) tail at the 3' end of SEQ ID NO:179; and

- (ab) the nucleotide sequence of the cDNA insert of clone BN387\_3 deposited with the ATCC under accession number 98292;

- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

- (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:

- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (ba) SEQ ID NO:179, but excluding the poly(A) tail at the 3' end of SEQ ID NO:179; and

- (bb) the nucleotide sequence of the cDNA insert of clone BN387\_3 deposited with the ATCC under accession number 98292;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and

- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:179, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:179 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:179, but excluding the poly(A) tail at the 3' end of SEQ ID NO:179. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:179 from nucleotide 751 to nucleotide 906, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:179 from nucleotide 751 to nucleotide 906, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:179 from nucleotide 751 to nucleotide 906. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:179 from nucleotide 829 to nucleotide 906, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:179 from nucleotide 829 to nucleotide 906, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:179 from nucleotide 829 to nucleotide 906. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:179 from nucleotide 556 to nucleotide 831, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:179 from nucleotide 556 to nucleotide 831, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:179 from nucleotide 556 to nucleotide 831.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:180;
- (b) the amino acid sequence of SEQ ID NO:180 from amino acid 1 to amino acid 27;
- (c) a fragment of the amino acid sequence of SEQ ID NO:180, the fragment comprising eight contiguous amino acids of SEQ ID NO:180; and
- (d) the amino acid sequence encoded by the cDNA insert of clone BN387\_3 deposited with the ATCC under accession number 98292;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:180 or the amino acid sequence of SEQ ID NO:180 from amino acid 1 to amino acid 27. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:180 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:180, or a protein



comprising a fragment of the amino acid sequence of SEQ ID NO:180 having biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:180.

In one embodiment, the present invention provides a composition comprising an isolated  
5 polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:181;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:181 from nucleotide 139 to nucleotide 765;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:181  
10 from nucleotide 1 to nucleotide 416;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BQ135\_2 deposited with the ATCC under accession number 98292;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA  
15 insert of clone BQ135\_2 deposited with the ATCC under accession number 98292;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BQ135\_2 deposited with the ATCC under accession number 98292;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert  
20 of clone BQ135\_2 deposited with the ATCC under accession number 98292;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:182;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:182 having biological activity, the fragment comprising  
25 eight contiguous amino acids of SEQ ID NO:182;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of  
30 the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:181.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:181 from nucleotide 139 to nucleotide 765; the nucleotide sequence of SEQ ID NO:181 from nucleotide 1 to nucleotide 416; the nucleotide sequence of the full-length protein coding sequence of clone BQ135\_2 deposited with the ATCC under accession number 98292; or the nucleotide  
5 sequence of a mature protein coding sequence of clone BQ135\_2 deposited with the ATCC under accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BQ135\_2 deposited with the ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID  
10 NO:182 from amino acid 1 to amino acid 93. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:182 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:182, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ  
15 ID NO:182 having biological activity, the fragment comprising the amino acid sequence from amino acid 99 to amino acid 108 of SEQ ID NO:182.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:181.

Further embodiments of the invention provide isolated polynucleotides produced  
20 according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:  
25 (aa) SEQ ID NO:181, but excluding the poly(A) tail at the 3' end of SEQ ID NO:181; and  
(ab) the nucleotide sequence of the cDNA insert of clone BQ135\_2 deposited with the ATCC under accession number 98292;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions  
30 at least as stringent as 4X SSC at 50 degrees C; and  
(iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:181, but excluding the poly(A) tail at the 3' end of SEQ ID NO:181; and

(bb) the nucleotide sequence of the cDNA insert of clone BQ135\_2 deposited with the ATCC under accession number 98292;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

10 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:181, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:181 to a nucleotide  
15 sequence corresponding to the 3' end of SEQ ID NO:181, but excluding the poly(A) tail at the 3' end of SEQ ID NO:181. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:181 from nucleotide 139 to nucleotide 765, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:181 from nucleotide 139 to nucleotide  
20 765, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:181 from nucleotide 139 to nucleotide 765. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:181 from nucleotide 1 to nucleotide 416, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:181 from nucleotide 1 to  
25 nucleotide 416, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:181 from nucleotide 1 to nucleotide 416.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:182;  
30 (b) the amino acid sequence of SEQ ID NO:182 from amino acid 1 to amino acid 93;

(c) a fragment of the amino acid sequence of SEQ ID NO:182, the fragment comprising eight contiguous amino acids of SEQ ID NO:182; and

(d) the amino acid sequence encoded by the cDNA insert of clone BQ135\_2  
35 deposited with the ATCC under accession number 98292;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:182 or the amino acid sequence of SEQ ID NO:182 from amino acid 1 to amino acid 93. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID

5 NO:182 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:182, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:182 having biological activity, the fragment comprising the amino acid sequence from amino acid 99 to amino acid 108 of SEQ ID NO:182.

10 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:183;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:183 from nucleotide 214 to nucleotide 714;
- 15 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:183 from nucleotide 151 to nucleotide 531;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CR678\_1 deposited with the ATCC under accession number 98292;
- 20 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CR678\_1 deposited with the ATCC under accession number 98292;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CR678\_1 deposited with the ATCC under accession number 98292;
- 25 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CR678\_1 deposited with the ATCC under accession number 98292;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:184;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:184 having biological activity, the fragment comprising
- 30 eight contiguous amino acids of SEQ ID NO:184;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h)
- 35 or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:183.

5 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:183 from nucleotide 214 to nucleotide 714; the nucleotide sequence of SEQ ID NO:183 from nucleotide 151 to nucleotide 531; the nucleotide sequence of the full-length protein coding sequence of clone CR678\_1 deposited with the ATCC under accession number 98292; or the  
10 nucleotide sequence of a mature protein coding sequence of clone CR678\_1 deposited with the ATCC under accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CR678\_1 deposited with the ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid  
15 sequence of SEQ ID NO:184 from amino acid 1 to amino acid 106. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:184 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:184, or a polynucleotide encoding a protein comprising a fragment of the  
20 amino acid sequence of SEQ ID NO:184 having biological activity, the fragment comprising the amino acid sequence from amino acid 78 to amino acid 87 of SEQ ID NO:184.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:183.

Further embodiments of the invention provide isolated polynucleotides produced  
25 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (aa) SEQ ID NO:183, but excluding the poly(A) tail at the 3' end of SEQ ID NO:183; and

(ab) the nucleotide sequence of the cDNA insert of clone CR678\_1 deposited with the ATCC under accession number 98292;

(ii) hybridizing said probe(s) to human genomic DNA in conditions  
35 at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in

5 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:183, but excluding the poly(A) tail at the 3' end of SEQ ID NO:183; and

10 (bb) the nucleotide sequence of the cDNA insert of clone CR678\_1 deposited with the ATCC under accession number 98292;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

15 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:183, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:183 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:183, but excluding the poly(A) tail at the 3' end of SEQ ID NO:183. Also preferably the polynucleotide isolated according to the above  
20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:183 from nucleotide 214 to nucleotide 714, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:183 from nucleotide 214 to nucleotide 714, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:183 from nucleotide 214 to nucleotide 714. Also preferably the polynucleotide isolated according to  
25 the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:183 from nucleotide 151 to nucleotide 531, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:183 from nucleotide 151 to nucleotide 531, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:183 from nucleotide 151 to nucleotide 531.

30 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:184;

(b) the amino acid sequence of SEQ ID NO:184 from amino acid 1 to amino acid 106;

(c) a fragment of the amino acid sequence of SEQ ID NO:184, the fragment comprising eight contiguous amino acids of SEQ ID NO:184; and

(d) the amino acid sequence encoded by the cDNA insert of clone CR678\_1 deposited with the ATCC under accession number 98292;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:184 or the amino acid sequence of SEQ ID NO:184 from amino acid 1 to amino acid 106. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:184 having biological activity, the fragment preferably comprising eight (more preferably  
10 twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:184, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:184 having biological activity, the fragment comprising the amino acid sequence from amino acid 78 to amino acid 87 of SEQ ID NO:184.

In one embodiment, the present invention provides a composition comprising an isolated  
15 polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:185;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:185 from nucleotide 116 to nucleotide 4498;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:185  
20 from nucleotide 1221 to nucleotide 1711;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CW420\_2 deposited with the ATCC under accession number 98292;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA  
25 insert of clone CW420\_2 deposited with the ATCC under accession number 98292;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CW420\_2 deposited with the ATCC under accession number 98292;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert  
30 of clone CW420\_2 deposited with the ATCC under accession number 98292;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:186;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:186 having biological activity, the fragment comprising  
35 eight contiguous amino acids of SEQ ID NO:186;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:185.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:185 from nucleotide 116 to nucleotide 4498; the nucleotide sequence of SEQ ID NO:185 from nucleotide 1221 to nucleotide 1711; the nucleotide sequence of the full-length protein coding sequence of clone CW420\_2 deposited with the ATCC under accession number 98292; or the nucleotide sequence of a mature protein coding sequence of clone CW420\_2 deposited with the  
15 ATCC under accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CW420\_2 deposited with the ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:186 from amino acid 370 to amino acid 532. In further preferred  
20 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:186 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:186, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:186 having biological activity, the fragment comprising the  
25 amino acid sequence from amino acid 725 to amino acid 734 of SEQ ID NO:186.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:185.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

30 (a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:185, but excluding the poly(A) tail at the 3'  
35 end of SEQ ID NO:185; and



- (ab) the nucleotide sequence of the cDNA insert of clone CW420\_2 deposited with the ATCC under accession number 98292;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group
- 10 consisting of:
- (ba) SEQ ID NO:185, but excluding the poly(A) tail at the 3' end of SEQ ID NO:185; and
- (bb) the nucleotide sequence of the cDNA insert of clone CW420\_2 deposited with the ATCC under accession number 98292;
- 15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide

20 sequence corresponding to the cDNA sequence of SEQ ID NO:185, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:185 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:185, but excluding the poly(A) tail at the 3' end of SEQ ID NO:185. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:185

25 from nucleotide 116 to nucleotide 4498, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:185 from nucleotide 116 to nucleotide 4498, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:185 from nucleotide 116 to nucleotide 4498. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of

30 SEQ ID NO:185 from nucleotide 1221 to nucleotide 1711, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:185 from nucleotide 1221 to nucleotide 1711, to a nucleotide sequence corresponding to the 3' end of said sequence f SEQ ID NO:185 from nucleotide 1221 to nucleotide 1711.

In other embodiments, the present invention provides a composition comprising a protein,

35 wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:186;
- (b) the amino acid sequence of SEQ ID NO:186 from amino acid 370 to amino acid 532;
- (c) a fragment of the amino acid sequence of SEQ ID NO:186, the fragment comprising eight contiguous amino acids of SEQ ID NO:186; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CW420\_2 deposited with the ATCC under accession number 98292;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:186 or the amino acid sequence of SEQ ID NO:186 from amino acid 370 to amino acid 532. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:186 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:186, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:186 having biological activity, the fragment comprising the amino acid sequence from amino acid 725 to amino acid 734 of SEQ ID NO:186.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:187;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:187 from nucleotide 119 to nucleotide 2176;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:187 from nucleotide 1 to nucleotide 529;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CW795\_2 deposited with the ATCC under accession number 98292;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CW795\_2 deposited with the ATCC under accession number 98292;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CW795\_2 deposited with the ATCC under accession number 98292;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CW795\_2 deposited with the ATCC under accession number 98292;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:188;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:188 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:188;

5 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

10 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:187.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:187 from nucleotide 119 to nucleotide 2176; the nucleotide sequence of SEQ ID NO:187 from  
15 nucleotide 1 to nucleotide 529; the nucleotide sequence of the full-length protein coding sequence of clone CW795\_2 deposited with the ATCC under accession number 98292; or the nucleotide sequence of a mature protein coding sequence of clone CW795\_2 deposited with the ATCC under accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CW795\_2 deposited with the  
20 ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:188 from amino acid 1 to amino acid 137. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:188 having biological activity, the fragment preferably comprising eight  
25 (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:188, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:188 having biological activity, the fragment comprising the amino acid sequence from amino acid 338 to amino acid 347 of SEQ ID NO:188.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID  
30 NO:187.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:187, but excluding the poly(A) tail at the 3' end of SEQ ID NO:187; and

(ab) the nucleotide sequence of the cDNA insert of clone CW795\_2 deposited with the ATCC under accession number 98292;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:187, but excluding the poly(A) tail at the 3' end of SEQ ID NO:187; and

(bb) the nucleotide sequence of the cDNA insert of clone CW795\_2 deposited with the ATCC under accession number 98292;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:187, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:187 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:187, but excluding the poly(A) tail at the 3' end of SEQ ID NO:187. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:187 from nucleotide 119 to nucleotide 2176, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:187 from nucleotide 119 to nucleotide 2176, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:187 from nucleotide 119 to nucleotide 2176. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:187 from nucleotide 1 to nucleotide 529, and extending contiguously from a

nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:187 from nucleotide 1 to nucleotide 529, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:187 from nucleotide 1 to nucleotide 529.

In other embodiments, the present invention provides a composition comprising a protein,  
5 wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:188;
- (b) the amino acid sequence of SEQ ID NO:188 from amino acid 1 to amino acid 137;
- (c) a fragment of the amino acid sequence of SEQ ID NO:188, the fragment  
10 comprising eight contiguous amino acids of SEQ ID NO:188; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CW795\_2 deposited with the ATCC under accession number 98292;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:188 or the amino acid sequence of SEQ ID  
15 NO:188 from amino acid 1 to amino acid 137. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:188 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:188, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:188 having biological activity,  
20 the fragment comprising the amino acid sequence from amino acid 338 to amino acid 347 of SEQ ID NO:188.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:189;
- 25 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:189 from nucleotide 401 to nucleotide 589;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:189 from nucleotide 258 to nucleotide 627;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length  
30 protein coding sequence of clone CW823\_3 deposited with the ATCC under accession number 98292;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CW823\_3 deposited with the ATCC under accession number 98292;

- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CW823\_3 deposited with the ATCC under accession number 98292;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CW823\_3 deposited with the ATCC under accession number 98292;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:190;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:190 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:190;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:189.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:189 from nucleotide 401 to nucleotide 589; the nucleotide sequence of SEQ ID NO:189 from nucleotide 258 to nucleotide 627; the nucleotide sequence of the full-length protein coding sequence of clone CW823\_3 deposited with the ATCC under accession number 98292; or the nucleotide sequence of a mature protein coding sequence of clone CW823\_3 deposited with the ATCC under accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CW823\_3 deposited with the ATCC under accession number 98292. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:190 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:190, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:190 having biological activity, the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID NO:190.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:189.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:189, but excluding the poly(A) tail at the 3' end of SEQ ID NO:189; and

(ab) the nucleotide sequence of the cDNA insert of clone CW823\_3 deposited with the ATCC under accession number 98292;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:189, but excluding the poly(A) tail at the 3' end of SEQ ID NO:189; and

(bb) the nucleotide sequence of the cDNA insert of clone CW823\_3 deposited with the ATCC under accession number 98292;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:189, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:189 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:189, but excluding the poly(A) tail at the 3' end of SEQ ID NO:189. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:189 from nucleotide 401 to nucleotide 589, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:189 from nucleotide 401 to nucleotide 589, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:189

from nucleotide 401 to nucleotide 589. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:189 from nucleotide 258 to nucleotide 627, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:189 from nucleotide 258 to nucleotide 627, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:189 from nucleotide 258 to nucleotide 627.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:190;
- 10 (b) a fragment of the amino acid sequence of SEQ ID NO:190, the fragment comprising eight contiguous amino acids of SEQ ID NO:190; and
- (c) the amino acid sequence encoded by the cDNA insert of clone CW823\_3 deposited with the ATCC under accession number 98292;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:190. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:190 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:190, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:190 having biological activity, the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID NO:190.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:191;
- 25 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:191 from nucleotide 548 to nucleotide 868;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:191 from nucleotide 590 to nucleotide 868;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone DF989\_3 deposited with the ATCC under accession number 98292;
- 30 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone DF989\_3 deposited with the ATCC under accession number 98292;



- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone DF989\_3 deposited with the ATCC under accession number 98292;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone DF989\_3 deposited with the ATCC under accession number 98292;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:192;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:192 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:192;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:191.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:191 from nucleotide 548 to nucleotide 868; the nucleotide sequence of SEQ ID NO:191 from nucleotide 590 to nucleotide 868; the nucleotide sequence of the full-length protein coding sequence of clone DF989\_3 deposited with the ATCC under accession number 98292; or the nucleotide sequence of a mature protein coding sequence of clone DF989\_3 deposited with the ATCC under accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone DF989\_3 deposited with the ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:192 from amino acid 75 to amino acid 107. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:192 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:192, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:192 having biological activity, the fragment comprising the amino acid sequence from amino acid 48 to amino acid 57 of SEQ ID NO:192.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:191 and SEQ ID NO:193.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5                   (a)     a process comprising the steps of:
- (i)     preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa)   SEQ ID NO:191;
- 10                   (ab)   SEQ ID NO:193, but excluding the poly(A) tail at the 3' end of SEQ ID NO:193; and
- (ac)   the nucleotide sequence of the cDNA insert of clone DF989\_3 deposited with the ATCC under accession number 98292;
- (ii)    hybridizing said probe(s) to human genomic DNA in conditions
- 15                   at least as stringent as 4X SSC at 50 degrees C; and
- (iii)   isolating the DNA polynucleotides detected with the probe(s);
- and
- (b)     a process comprising the steps of:
- (i)     preparing one or more polynucleotide primers that hybridize in
- 20                   6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba)   SEQ ID NO:191;
- (bb)   SEQ ID NO:193, but excluding the poly(A) tail at the 3' end of SEQ ID NO:193; and
- 25                   (bc)   the nucleotide sequence of the cDNA insert of clone DF989\_3 deposited with the ATCC under accession number 98292;
- (ii)    hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii)   amplifying human DNA sequences; and
- 30                   (iv)   isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:191 and SEQ ID NO:193, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:191 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:193, but excluding

35   the poly(A) tail at the 3' end of SEQ ID NO:193. Also preferably the polynucleotide isolated

according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:191, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:191 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:191. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:191 from nucleotide 548 to nucleotide 868, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:191 from nucleotide 548 to nucleotide 868, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:191 from nucleotide 548 to nucleotide 868. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:191 from nucleotide 590 to nucleotide 868, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:191 from nucleotide 590 to nucleotide 868, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:191 from nucleotide 590 to nucleotide 868.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:192;
- (b) the amino acid sequence of SEQ ID NO:192 from amino acid 75 to amino acid 107;
- (c) a fragment of the amino acid sequence of SEQ ID NO:192, the fragment comprising eight contiguous amino acids of SEQ ID NO:192; and
- (d) the amino acid sequence encoded by the cDNA insert of clone DF989\_3 deposited with the ATCC under accession number 98292;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:192 or the amino acid sequence of SEQ ID NO:192 from amino acid 75 to amino acid 107. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:192 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:192, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:192 having biological activity, the fragment comprising the amino acid sequence from amino acid 48 to amino acid 57 of SEQ ID NO:192.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:194;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:194 from nucleotide 251 to nucleotide 787;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:194 from nucleotide 371 to nucleotide 787;
- 5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone DL162\_1 deposited with the ATCC under accession number 98292;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone DL162\_1 deposited with the ATCC under accession number 98292;
- 10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone DL162\_1 deposited with the ATCC under accession number 98292;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone DL162\_1 deposited with the ATCC under accession number 98292;
- 15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:195;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:195 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:195;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of
- 25 the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:194.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:194

30 from nucleotide 251 to nucleotide 787; the nucleotide sequence of SEQ ID NO:194 from nucleotide 371 to nucleotide 787; the nucleotide sequence of the full-length protein coding sequence of clone DL162\_1 deposited with the ATCC under accession number 98292; or the nucleotide sequence of a mature protein coding sequence of clone DL162\_1 deposited with the ATCC under accession number 98292. In other preferred embodiments, the polynucleotide

35 encodes the full-length or a mature protein encoded by the cDNA insert of clone DL162\_1

deposited with the ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:195 from amino acid 38 to amino acid 170. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a  
5 fragment of the amino acid sequence of SEQ ID NO:195 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:195, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:195 having biological activity, the fragment comprising the amino acid sequence from amino acid 84 to amino acid 93 of SEQ ID NO:195.

10 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:194.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - 15 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:194, but excluding the poly(A) tail at the 3' end of SEQ ID NO:194; and
    - 20 (ab) the nucleotide sequence of the cDNA insert of clone DL162\_1 deposited with the ATCC under accession number 98292;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - (iii) isolating the DNA polynucleotides detected with the probe(s);
    - 25 and
  - (b) a process comprising the steps of:
    - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
      - 30 (ba) SEQ ID NO:194, but excluding the poly(A) tail at the 3' end of SEQ ID NO:194; and
      - (bb) the nucleotide sequence of the cDNA insert of clone DL162\_1 deposited with the ATCC under accession number 98292;
      - (ii) hybridizing said primer(s) to human genomic DNA in conditions
      - 35 at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:194, and extending contiguously  
5 from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:194 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:194, but excluding the poly(A) tail at the 3' end of SEQ ID NO:194. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:194 from nucleotide 251 to nucleotide 787, and extending contiguously from a nucleotide sequence  
10 corresponding to the 5' end of said sequence of SEQ ID NO:194 from nucleotide 251 to nucleotide 787, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:194 from nucleotide 251 to nucleotide 787. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:194 from nucleotide 371 to nucleotide 787, and extending contiguously from a nucleotide  
15 sequence corresponding to the 5' end of said sequence of SEQ ID NO:194 from nucleotide 371 to nucleotide 787, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:194 from nucleotide 371 to nucleotide 787.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 20 (a) the amino acid sequence of SEQ ID NO:195;
- (b) the amino acid sequence of SEQ ID NO:195 from amino acid 38 to amino acid 170;
- (c) a fragment of the amino acid sequence of SEQ ID NO:195, the fragment comprising eight contiguous amino acids of SEQ ID NO:195; and
- 25 (d) the amino acid sequence encoded by the cDNA insert of clone DL162\_1 deposited with the ATCC under accession number 98292;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:195 or the amino acid sequence of SEQ ID NO:195 from amino acid 38 to amino acid 170. In further preferred embodiments, the present  
30 invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:195 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:195, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:195 having biological activity, the fragment comprising the amino acid sequence from amino acid 84 to amino acid 93 of SEQ  
35 ID NO:195.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:196;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:196  
5 from nucleotide 121 to nucleotide 3345;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:196  
from nucleotide 160 to nucleotide 3345;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:196  
from nucleotide 2592 to nucleotide 3318;
- 10 (e) a polynucleotide comprising the nucleotide sequence of the full-length  
protein coding sequence of clone DL162\_2 deposited with the ATCC under accession  
number 98292;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA  
insert of clone DL162\_2 deposited with the ATCC under accession number 98292;
- 15 (g) a polynucleotide comprising the nucleotide sequence of a mature protein  
coding sequence of clone DL162\_2 deposited with the ATCC under accession number  
98292;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert  
of clone DL162\_2 deposited with the ATCC under accession number 98292;
- 20 (i) a polynucleotide encoding a protein comprising the amino acid sequence  
of SEQ ID NO:197;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino  
acid sequence of SEQ ID NO:197 having biological activity, the fragment comprising  
eight contiguous amino acids of SEQ ID NO:197;
- 25 (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h)  
above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i)  
or (j) above ;
- (m) a polynucleotide that hybridizes under stringent conditions to any one of  
30 the polynucleotides specified in (a)-(j); and
- (n) a polynucleotide that hybridizes under stringent conditions to any one of  
the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the  
length of SEQ ID NO:196.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:196  
35 from nucleotide 121 to nucleotide 3345; the nucleotide sequence of SEQ ID NO:196 from

nucleotide 160 to nucleotide 3345; the nucleotide sequence of SEQ ID NO:196 from nucleotide 2592 to nucleotide 3318; the nucleotide sequence of the full-length protein coding sequence of clone DL162\_2 deposited with the ATCC under accession number 98292; or the nucleotide sequence of a mature protein coding sequence of clone DL162\_2 deposited with the ATCC under  
5 accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone DL162\_2 deposited with the ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID  
10 NO:197 from amino acid 860 to amino acid 1066. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:197 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:197, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:197 having biological activity, the fragment comprising the amino acid sequence from  
15 amino acid 532 to amino acid 541 of SEQ ID NO:197.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:196.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 20 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:196, but excluding the poly(A) tail at the 3'  
25 end of SEQ ID NO:196; and
- (ab) the nucleotide sequence of the cDNA insert of clone DL162\_2 deposited with the ATCC under accession number 98292;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 30 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group  
35 consisting of:



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(ba) SEQ ID NO:196, but excluding the poly(A) tail at the 3' end of SEQ ID NO:196; and

(bb) the nucleotide sequence of the cDNA insert of clone DL162\_2 deposited with the ATCC under accession number 98292;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide  
10 sequence corresponding to the cDNA sequence of SEQ ID NO:196, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:196 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:196, but excluding the poly(A) tail at the 3' end of SEQ ID NO:196. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:196  
15 from nucleotide 121 to nucleotide 3345, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:196 from nucleotide 121 to nucleotide 3345, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:196 from nucleotide 121 to nucleotide 3345. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of  
20 SEQ ID NO:196 from nucleotide 160 to nucleotide 3345, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:196 from nucleotide 160 to nucleotide 3345, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:196 from nucleotide 160 to nucleotide 3345. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence  
25 corresponding to the cDNA sequence of SEQ ID NO:196 from nucleotide 2592 to nucleotide 3318, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:196 from nucleotide 2592 to nucleotide 3318, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:196 from nucleotide 2592 to nucleotide 3318.

30 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:197;

(b) the amino acid sequence of SEQ ID NO:197 from amino acid 860 to amino acid 1066;

(c) a fragment of the amino acid sequence of SEQ ID NO:197, the fragment comprising eight contiguous amino acids of SEQ ID NO:197; and

(d) the amino acid sequence encoded by the cDNA insert of clone DL162\_2 deposited with the ATCC under accession number 98292;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:197 or the amino acid sequence of SEQ ID NO:197 from amino acid 860 to amino acid 1066. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:197 having biological activity, the fragment preferably comprising eight (more preferably  
10 twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:197, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:197 having biological activity, the fragment comprising the amino acid sequence from amino acid 532 to amino acid 541 of SEQ ID NO:197.

In one embodiment, the present invention provides a composition comprising an isolated  
15 polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:198;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:198 from nucleotide 117 to nucleotide 2600;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:198  
20 from nucleotide 2130 to nucleotide 2600;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:198 from nucleotide 1 to nucleotide 506;

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone EC172\_1 deposited with the ATCC under accession  
25 number 98292;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone EC172\_1 deposited with the ATCC under accession number 98292;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone EC172\_1 deposited with the ATCC under accession number  
30 98292;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone EC172\_1 deposited with the ATCC under accession number 98292;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:199;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:199 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:199;

5 (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

10 (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:198.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:198 from nucleotide 117 to nucleotide 2600; the nucleotide sequence of SEQ ID NO:198 from  
15 nucleotide 2130 to nucleotide 2600; the nucleotide sequence of SEQ ID NO:198 from nucleotide 1 to nucleotide 506; the nucleotide sequence of the full-length protein coding sequence of clone EC172\_1 deposited with the ATCC under accession number 98292; or the nucleotide sequence of a mature protein coding sequence of clone EC172\_1 deposited with the ATCC under accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a  
20 mature protein encoded by the cDNA insert of clone EC172\_1 deposited with the ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:199 from amino acid 1 to amino acid 130. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ  
25 ID NO:199 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:199, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:199 having biological activity, the fragment comprising the amino acid sequence from amino acid 409 to amino acid 418 of SEQ ID NO:199.

30 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:198.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (aa) SEQ ID NO:198, but excluding the poly(A) tail at the 3' end of SEQ ID NO:198; and

(ab) the nucleotide sequence of the cDNA insert of clone EC172\_1 deposited with the ATCC under accession number 98292;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

10 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:198, but excluding the poly(A) tail at the 3' end of SEQ ID NO:198; and

(bb) the nucleotide sequence of the cDNA insert of clone EC172\_1 deposited with the ATCC under accession number 98292;

20 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide  
25 sequence corresponding to the cDNA sequence of SEQ ID NO:198, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:198 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:198, but excluding the poly(A) tail at the 3' end of SEQ ID NO:198. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:198  
30 from nucleotide 117 to nucleotide 2600, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:198 from nucleotide 117 to nucleotide 2600, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:198 from nucleotide 117 to nucleotide 2600. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of  
35 SEQ ID NO:198 from nucleotide 2130 to nucleotide 2600, and extending contiguously from a

nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:198 from nucleotide 2130 to nucleotide 2600, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:198 from nucleotide 2130 to nucleotide 2600. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence  
5 corresponding to the cDNA sequence of SEQ ID NO:198 from nucleotide 1 to nucleotide 506, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:198 from nucleotide 1 to nucleotide 506, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:198 from nucleotide 1 to nucleotide 506.

In other embodiments, the present invention provides a composition comprising a protein,  
10 wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:199;
- (b) the amino acid sequence of SEQ ID NO:199 from amino acid 1 to amino acid 130;
- (c) a fragment of the amino acid sequence of SEQ ID NO:199, the fragment  
15 comprising eight contiguous amino acids of SEQ ID NO:199; and
- (d) the amino acid sequence encoded by the cDNA insert of clone EC172\_1 deposited with the ATCC under accession number 98292;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:199 or the amino acid sequence of SEQ ID  
20 NO:199 from amino acid 1 to amino acid 130. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:199 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:199, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:199 having biological activity,  
25 the fragment comprising the amino acid sequence from amino acid 409 to amino acid 418 of SEQ ID NO:199.

In certain preferred embodiments, the polynucleotide is operably linked to an expression control sequence. The invention also provides a host cell, including bacterial, yeast, insect and mammalian cells, transformed with such polynucleotide compositions. Also provided by the  
30 present invention are organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein.

Processes are also provided for producing a protein, which comprise:

- (a) growing a culture of the host cell transformed with such polynucleotide compositions in a suitable culture medium; and
- 35 (b) purifying the protein from the culture.

The protein produced according to such methods is also provided by the present invention.

Protein compositions of the present invention may further comprise a pharmaceutically acceptable carrier. Compositions comprising an antibody which specifically reacts with such protein are also provided by the present invention.

5       Methods are also provided for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically effective amount of a composition comprising a protein of the present invention and a pharmaceutically acceptable carrier.

10                               **BRIEF DESCRIPTION OF THE DRAWINGS**

Figures 1A and 1B are schematic representations of the pED6 and pNOTs vectors, respectively, used for deposit of clones disclosed herein.

**DETAILED DESCRIPTION**

15   **ISOLATED PROTEINS AND POLYNUCLEOTIDES**

Nucleotide and amino acid sequences, as presently determined, are reported below for each clone and protein disclosed in the present application. The nucleotide sequence of each clone can readily be determined by sequencing of the deposited clone in accordance with known methods. The predicted amino acid sequence (both full-length and mature forms) can then be  
20   determined from such nucleotide sequence. The amino acid sequence of the protein encoded by a particular clone can also be determined by expression of the clone in a suitable host cell, collecting the protein and determining its sequence. For each disclosed protein applicants have identified what they have determined to be the reading frame best identifiable with sequence information available at the time of filing.

25       As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported  
30   across the membrane of the endoplasmic reticulum.

**Clone "AX65\_22"**

A polynucleotide of the present invention has been identified as clone "AX65\_22". AX65\_22 was isolated from a human adult testes cDNA library using methods which are selective  
35   for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding

a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. AX65\_22 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AX65\_22 protein").

5 The nucleotide sequence of the 5' portion of AX65\_22 as presently determined is reported in SEQ ID NO:1. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:2. The predicted amino acid sequence of the AX65\_22 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:2. Amino acids 8 to 20 of SEQ ID NO:2 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 21. Due to the hydrophobic nature of the predicted  
10 leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the AX65\_22 protein. Additional nucleotide sequence from the 3' portion of AX65\_22, including a poly(A) tail, is reported in SEQ ID NO:3.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
15 AX65\_22 should be approximately 3500 bp.

The nucleotide sequence disclosed herein for AX65\_22 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. AX65\_22 demonstrated at least some similarity with sequences identified as T08476 (Eukaryotic expression vector pAPEX-3p) and U46493 (Cloning vector pFlp recombinase  
20 gene, complete cds). The predicted AX65\_22 protein demonstrated at least some homology with sequences identified as J01969 (DNA polymerase [Human adenovirus type 5]), R07640 (Deduced protein sequence of p170-2 comprising T4), and X57205 (fibroblast growth factor receptor [Homo sapiens]). Based upon sequence similarity, AX65\_22 proteins and each similar protein or peptide may share at least  
25 some activity.

#### Clone "BD335\_14"

A polynucleotide of the present invention has been identified as clone "BD335\_14". BD335\_14 was isolated from a human fetal kidney cDNA library using methods which are  
30 selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BD335\_14 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BD335\_14 protein").

The nucleotide sequence of BD335\_14 as presently determined is reported in SEQ ID  
35 NO:4, and includes a poly(A) tail. What applicants presently believe to be the proper reading

frame and the predicted amino acid sequence of the BD335\_14 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:5.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BD335\_14 should be approximately 3000 bp.

5       The nucleotide sequence disclosed herein for BD335\_14 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. The predicted BD335\_14 protein demonstrated at least some similarity with sequences identified as U83511 (APXL [Homo sapiens]). Based upon sequence similarity, BD335\_14 proteins and each homologous protein or peptide may share at least some activity. The  
10   TopPredII computer program predicts three potential transmembrane domains within the BD335\_14 protein sequence, one centered around amino acid 80, another around amino acid 320, and a third around amino acid 700 of SEQ ID NO:5.

Clone "BG241\_1"

15       A polynucleotide of the present invention has been identified as clone "BG241\_1". BG241\_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BG241\_1 is a full-length clone, including the entire coding sequence of  
20   a secreted protein (also referred to herein as "BG241\_1 protein").

The nucleotide sequence of the 5' portion of BG241\_1 as presently determined is reported in SEQ ID NO:6. An additional internal nucleotide sequence from BG241\_1 as presently determined is reported in SEQ ID NO:7. What applicants believe is the proper reading frame and the predicted amino acid sequence encoded by such internal sequence is reported in SEQ ID NO:8.

25   Additional nucleotide sequence from the 3' portion of BG241\_1, including a poly(A) tail, is reported in SEQ ID NO:9.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BG241\_1 should be approximately 800 bp.

The nucleotide sequence disclosed herein for BG241\_1 was searched against the GenBank  
30   and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BG241\_1 demonstrated at least some similarity with sequences identified as AI082187(ox75f01.x1 Soares\_NhHMPu\_S1 Homo sapiens cDNA clone IMAGE 1662169 3' similar to contains element MSR1 repetitive element; mRNA sequence), W38781 (zb27g08.r1 Soares parathyroid tumor NbHPA Homo sapiens), and Y12781 (Homo sapiens  
35   mRNA for transducin (beta) like 1 protein). The predicted BG241\_1 protein demonstrated at



least some similarity to sequences identified as Y12781 (transducin (beta) like 1 protein [Homo sapiens]) and other beta-transducin-like proteins (see GenBank accession numbers L28125 and T86738). Based upon sequence similarity, BG241\_1 proteins and each similar protein or peptide may share at least some activity.

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Clone "BL187\_4"

A polynucleotide of the present invention has been identified as clone "BL187\_4". BL187\_4 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding  
10 a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BL187\_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BL187\_4 protein").

The nucleotide sequence of BL187\_4 as presently determined is reported in SEQ ID NO:10, and includes a poly(A) tail. What applicants presently believe to be the proper reading  
15 frame and the predicted amino acid sequence of the BL187\_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:11. Amino acids 17 to 29 of SEQ ID NO:11 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 30. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal  
20 sequence not be separated from the remainder of the BL187\_4 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BL187\_4 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for BL187\_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search  
25 protocols. BL187\_4 demonstrated at least some similarity with sequences identified as AA476210 (zw35g01.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 771312 3', mRNA sequence), AA868505 (ak43b04.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE 1408687 3' similar to SW PLZF\_HUMAN Q05516 ZINC FINGER PROTEIN PLZF; mRNA sequence), AA927876 (om18b09.s1 Soares NFL T GBC S1  
30 Homo sapiens cDNA clone IMAGE:1541369 3', mRNA sequence), AD000671 (Homo sapiens DNA from chromosome 19-cosmid f24109 containing HRX2, genomic sequence), H48938 (EST0010 Homo sapiens cDNA clone HTN-6-15), and Z63958 (H.sapiens CpG DNA, clone 93d10, forward read cpg93d10.f1a). The predicted amino acid sequence disclosed herein for BL187\_4 was searched against the GenPept and GeneSeq amino acid

sequence databases using the BLASTX search protocol. The predicted BL187\_4 protein demonstrated at least some similarity to sequences identified as R95242 (HIC-1 polypeptide), Z19002 (kruppel-like zinc finger protein [Homo sapiens]), and a number of other zinc-finger proteins. Based upon sequence similarity, BL187\_4 proteins and each similar protein or peptide may share at least some activity. Motifs analysis indicates the presence of two zinc-finger (C2H2 type) domains centered around amino acids 375 and 430 of SEQ ID NO:11, respectively. The TopPredII computer program predicts two potential transmembrane domains within the BL187\_4 protein sequence, one centered around amino acid 30 and another around amino acid 260 of SEQ ID NO:11. BL187\_4 protein appears to be a novel secreted or membrane-associated zinc-finger protein.

#### Clone "BL249\_18"

A polynucleotide of the present invention has been identified as clone "BL249\_18". BL249\_18 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BL249\_18 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BL249\_18 protein").

The nucleotide sequence of BL249\_18 as presently determined is reported in SEQ ID NO:12, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BL249\_18 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:13. Amino acids 32 to 44 of SEQ ID NO:13 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 45. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the BL249\_18 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BL249\_18 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for BL249\_18 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BL249\_18 demonstrated at least some similarity with sequences identified as AA034864 (mi53f01.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 467257 5'), AA115100 (zl02h12.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 491207 3'), AA219365 (zr04c06.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 650506 5'), AA399095 (zt59b06.r1 Soares

testis NHT Homo sapiens cDNA clone 726611 5'), R82633 (yj20a05.s1 Homo sapiens cDNA clone 149264 3'), and T22047 (Human gene signature HUMGS03590). The predicted amino acid sequence disclosed herein for BL249\_18 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted

5 BL249\_18 protein demonstrated at least some similarity to sequences identified as AC003673 (unknown protein (AAC09020.1) [Arabidopsis thaliana]) and Z98598 (hypothetical protein [Schizosaccharomyces pombe]). Based upon sequence similarity, BL249\_18 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the BL249\_18 protein sequence, one

10 centered around amino acid 45 and another around amino acid 680 of SEQ ID NO:13.

#### Clone "BO71\_1"

A polynucleotide of the present invention has been identified as clone "BO71\_1". BO71\_1 was isolated from a human adult retina cDNA library using methods which are selective

15 for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BO71\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BO71\_1 protein").

The nucleotide sequence of the 5' portion of BO71\_1 as presently determined is reported

20 in SEQ ID NO:14. An additional internal nucleotide sequence from BO71\_1 as presently determined is reported in SEQ ID NO:15. What applicants believe is the proper reading frame and the predicted amino acid sequence encoded by such internal sequence is reported in SEQ ID NO:16. Additional nucleotide sequence from the 3' portion of BO71\_1, including a poly(A) tail, is reported in SEQ ID NO:17.

25 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BO71\_1 should be approximately 2000 bp.

The nucleotide sequence disclosed herein for BO71\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BO71\_1 demonstrated at least some similarity with sequences identified as X86809

30 (H.sapiens mRNA for major astrocytic phosphoprotein PEA-15). The predicted amino acid sequence disclosed herein for BO71\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BO71\_1 protein demonstrated at least some similarity to sequences identified as U06144 (cellular disintegrin-related protein [Mus musculus]). Based upon sequence similarity, BO71\_1

35 proteins and each similar protein or peptide may share at least some activity.

Clone "BO365\_2"

A polynucleotide of the present invention has been identified as clone "BO365\_2". BO365\_2 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding  
5 a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BO365\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BO365\_2 protein").

The nucleotide sequence of BO365\_2 as presently determined is reported in SEQ ID NO:18, and includes a poly(A) tail. What applicants presently believe to be the proper reading  
10 frame and the predicted amino acid sequence of the BO365\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:19.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BO365\_2 should be approximately 2800 bp.

The nucleotide sequence disclosed herein for BO365\_2 was searched against the GenBank  
15 and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BO365\_2 demonstrated at least some similarity with sequences identified as D63876 (Human mRNA for KIAA0154 gene, partial cds) and Z83844 (Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 37E16; HTGS phase 1). The predicted amino acid sequence disclosed herein for BO365\_2 was searched against the GenPept and  
20 GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BO365\_2 protein demonstrated at least some similarity to sequences identified as D10250 (alpha-fetoprotein enhancer binding protein [Homo sapiens]), D63876 (KIAA0154 gene product is related to mouse gamma adaptin [Homo sapiens]), and R23962 (AFP-1). Based upon sequence similarity, BO365\_2 proteins and each similar protein or peptide may share at least  
25 some activity. The TopPredII computer program predicts three potential transmembrane domains within the BO365\_2 protein sequence, centered around amino acids 70, 140, and 180 of SEQ ID NO:19, respectively.

Clone "BV51\_1"

A polynucleotide of the present invention has been identified as clone "BV51\_1". BV51\_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding  
30 a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BV51\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BV51\_1 protein").  
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The nucleotide sequence of the 5' portion of BV51\_1 as presently determined is reported in SEQ ID NO:20. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:21. The predicted amino acid sequence of the BV51\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:21. Additional  
5 nucleotide sequence from the 3' portion of BV51\_1, including a poly(A) tail, is reported in SEQ ID NO:22.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BV51\_1 should be approximately 970 bp.

The nucleotide sequence disclosed herein for BV51\_1 was searched against the GenBank  
10 and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BV51\_1 demonstrated at least some similarity with sequences identified as AB012130 (Homo sapiens SBC2 mRNA for sodium bicarbonate cotransporter2, complete cds) and U46493 (Cloning vector pFlp recombinase gene, complete cds). The predicted amino acid sequence disclosed herein for BV51\_1 was searched against the GenPept and GeneSeq amino acid  
15 sequence databases using the BLASTX search protocol. The predicted BV51\_1 protein demonstrated at least some similarity to sequences identified as AB01213 (sodium bicarbonate cotransporter2 [Homo sapiens]). Based upon sequence similarity, BV51\_1 proteins and each similar protein or peptide may share at least some activity.

20        Clone "BV140\_3"

A polynucleotide of the present invention has been identified as clone "BV140\_3". BV140\_3 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence  
25 of the encoded protein. BV140\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BV140\_3 protein").

The nucleotide sequence of the 5' portion of BV140\_3 as presently determined is reported in SEQ ID NO:23. An additional internal nucleotide sequence from BV140\_3 as presently determined is reported in SEQ ID NO:24. What applicants believe is the proper reading frame  
30 and the predicted amino acid sequence encoded by such internal sequence is reported in SEQ ID NO:25. Additional nucleotide sequence from the 3' portion of BV140\_3, including a poly(A) tail, is reported in SEQ ID NO:26.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BV140\_3 should be approximately 3500 bp.

The nucleotide sequence disclosed herein for BV140\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BV140\_3 demonstrated at least some similarity with sequences identified as H72799 (yu07d10.r1 Homo sapiens cDNA clone 233107 5') and T94057 (ye33g08.r1 Homo sapiens cDNA clone 119582 5'). Based upon sequence similarity, BV140\_3 proteins and each similar protein or peptide may share at least some activity.

#### Clone "BV141\_2"

A polynucleotide of the present invention has been identified as clone "BV141\_2". BV141\_2 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BV141\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BV141\_2 protein").

The nucleotide sequence of BV141\_2 as presently determined is reported in SEQ ID NO:27, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BV141\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:28.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BV141\_2 should be approximately 1100 bp.

The nucleotide sequence disclosed herein for BV141\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BV141\_2 demonstrated at least some similarity with sequences identified as L26860 (Mus musculus (C6e) heavy chain immunoglobulin variable region gene). Based upon sequence similarity, BV141\_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the BV141\_2 protein sequence, one centered around amino acid 34 and another around amino acid 65 of SEQ ID NO:28. The nucleotide sequence of BV141\_2 indicates that it may contain one or more of the following repetitive element(s): L1 repeat.

#### Clone "CC194\_4"

A polynucleotide of the present invention has been identified as clone "CC194\_4". CC194\_4 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence

of the encoded protein. CC194\_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CC194\_4 protein").

The nucleotide sequence of the 5' portion of CC194\_4 as presently determined is reported in SEQ ID NO:29. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:30. The predicted amino acid sequence of the CC194\_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:30. Amino acids 88 to 100 of SEQ ID NO:30 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 101. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CC194\_4 protein. Additional nucleotide sequence from the 3' portion of CC194\_4, including a poly(A) tail, is reported in SEQ ID NO:31.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CC194\_4 should be approximately 3300 bp.

The nucleotide sequence disclosed herein for CC194\_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CC194\_4 demonstrated at least some similarity with sequences identified as AA722214 (zh20f10.s1 Soares pineal gland N3HPG Homo sapiens cDNA clone 412651 3', mRNA sequence), H11476 (ym10h08.s1 Homo sapiens cDNA clone 47781 3'), H11581 (ym10h08.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:47781 5' similar to SP:C36E8.3 CE00911; mRNA sequence), H23044 (ym51d07.r1 Homo sapiens cDNA clone 52058 5' similar to SP:C36E8.3 CE00911), N93789 (zb64g05.s1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 308408 3'), and W54544 (mc99a01.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus). The predicted amino acid sequence disclosed herein for CC194\_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CC194\_4 protein demonstrated at least some similarity to sequences identified as M38561 (CAD [Homo sapiens]). Based upon sequence similarity, CC194\_4 proteins and each similar protein or peptide may share at least some activity.

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#### Clone "DA136\_11"

A polynucleotide of the present invention has been identified as clone "DA136\_11". DA136\_11 was isolated from a human adult placenta cDNA library using methods which are

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selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. DA136\_11 includes at least a portion of the coding sequence of a secreted protein (also referred to herein as "DA136\_11 protein").

5       The nucleotide sequence of DA136\_11 as presently determined is reported in SEQ ID NO:32, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the DA136\_11 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:33.

      The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
10   DA136\_11 should be approximately 3800 bp.

      The nucleotide sequence disclosed herein for DA136\_11 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. DA136\_11 demonstrated at least some similarity with sequences identified as AA523414 (ng30a07.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA clone 936276), H89334  
15   (yw25h09.r1 Homo sapiens cDNA clone 253313 5'), R59925 (yh11b12.s1 Homo sapiens cDNA clone 42891 3), T66165 (Human interleukin-12 receptor alpha chain NR4 DNA), Y09328 (H.sapiens mRNA for IL13 receptor alpha-1 chain), and Y10659 (H.sapiens IL-13Ra mRNA). The predicted amino acid sequence disclosed herein for DA136\_11 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX  
20   search protocol. The predicted DA136\_11 protein demonstrated at least some similarity to sequences identified as L08960 (cell adhesion molecule [Gallus gallus]), M34083 (lactogen receptor precursor [Rattus norvegicus]), M59941 (GM-CSF receptor beta chain [Homo sapiens]), W09822 (Human interleukin-12 receptor alpha chain NR4), X61178 (interleukin-5 receptor type 3 [Homo sapiens]), and Y10659 (IL-13Ra [Homo sapiens]).  
25   Based upon sequence similarity, DA136\_11 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the DA136\_11 protein sequence, centered around amino acid 215 of SEQ ID NO:33.

30       Clone "AR415\_4"

      A polynucleotide of the present invention has been identified as clone "AR415\_4". AR415\_4 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence



of the encoded protein. AR415\_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AR415\_4 protein").

The nucleotide sequence of AR415\_4 as presently determined is reported in SEQ ID NO:34, and includes a poly(A) tail. What applicants presently believe to be the proper reading  
5 frame and the predicted amino acid sequence of the AR415\_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:35. Amino acids 14 to 26 of SEQ ID NO:35 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 27. Due to the hydrophobic nature of the predicted leader/signal  
10 sequence not be separated from the remainder of the AR415\_4 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AR415\_4 should be approximately 1500 bp.

The nucleotide sequence disclosed herein for AR415\_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search  
15 protocols. AR415\_4 demonstrated at least some similarity with sequences identified as AA100799 (zm26d01.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 526753 3'), AA100852 (zm26d01.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 526753 5' similar to SW CO02\_HUMAN P19075 TUMOR-ASSOCIATED ANTIGEN CO-029), AA146605 (zo35c09.r1 Stratagene colon (#937204) Homo sapiens cDNA clone 588880 5' similar to  
20 SW:CO02\_HUMAN P19075 TUMOR-ASSOCIATED ANTIGEN CO-029), AA224847 (nc33c12.s1 NCI CGAP Pr2 Homo sapiens cDNA clone 4079 similar to SW:CO02\_HUMAN P19075 TUMOR-ASSOCIATED ANTIGEN CO-029), AA225191 (nc21h08.s1 NCI CGAP Pr1 Homo sapiens cDNA clone 2968), AA593864 (nn19f08.s1 NCI CGAP Co12 Homo sapiens cDNA clone IMAGE:1084359), D26483 (Mouse mRNA for PE31/TALLA), M33680 (Human  
25 26-kDa cell surface protein TAPA-1 mRNA, complete cds), T14726 (Human CD53 antigen cDNA), and T23814 (Human gene signature HUMGS05723). The predicted amino acid sequence disclosed herein for AR415\_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted AR415\_4 protein demonstrated at least some sequence similarity with sequences identified as D29808 (TALLA-1  
30 [Homo sapiens]), M35252 (tumor-associated antigen [Homo sapiens]), and R22360 (CO-029 tumour associated antigen protein). Based upon sequence similarity, AR415\_4 proteins and each homologous protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the AR415\_4 protein sequence centered around amino acid 100 of SEQ ID NO:35.

Clone "AS63\_29"

A polynucleotide of the present invention has been identified as clone "AS63\_29". AS63\_29 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding  
5 a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. AS63\_29 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AS63\_29 protein").

The nucleotide sequence of the 5' portion of AS63\_29 as presently determined is reported in SEQ ID NO:36. What applicants presently believe is the proper reading frame for the coding  
10 region is indicated in SEQ ID NO:37. The predicted amino acid sequence of the AS63\_29 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:37. Amino acids 28 to 40 of SEQ ID NO:37 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 41. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted  
15 leader/signal sequence not be separated from the remainder of the AS63\_29 protein. Additional nucleotide sequence from the 3' portion of AS63\_29, including a poly(A) tail, is reported in SEQ ID NO:38.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AS63\_29 should be approximately 1700 bp.

20 The nucleotide sequence disclosed herein for AS63\_29 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. AS63\_29 demonstrated at least some similarity with sequences identified as L26877 (Mus musculus (B20c) heavy chain immunoglobulin variable region gene), T09146 (EST07039 Homo sapiens cDNA clone HIBBP68 5' end), T23466 (seq3050 Homo sapiens cDNA clone  
25 Hy18-Ch13-Charon40-cDNA-100 3'), and W55739 (ma35f05.r1 Life Tech mouse brain Mus musculus cDNA clone 312705 5'). The predicted amino acid sequence disclosed herein for AS63\_29 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted AS63\_29 protein demonstrated at least some sequence similarity with sequences identified as R04032 (Full length T4 encoded by plasmid  
30 pBG381). Based upon sequence similarity, AS63\_29 proteins and each homologous protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the AS63\_29 protein sequence, near the amino terminus.

Clone "AY304\_14"

A polynucleotide of the present invention has been identified as clone "AY304\_14". AY304\_14 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. AY304\_14 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AY304\_14 protein").

The nucleotide sequence of AY304\_14 as presently determined is reported in SEQ ID NO:39, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the AY304\_14 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:40.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AY304\_14 should be approximately 2200 bp.

The nucleotide sequence disclosed herein for AY304\_14 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. AY304\_14 demonstrated at least some similarity with sequences identified as AA127688 (zk92f05.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490305 3'), AA179609 (zp49g11.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 612836 5'), AA276253 (vc40f05.r1 Barstead MPLRB1 Mus musculus cDNA clone 777057 5'), H15545 (ym27d04.s1 Homo sapiens cDNA clone 49495 3' similar to contains PTR5 repetitive element), L08441 (Human autonomously replicating sequence (ARS) mRNA), N34949 (yy49h09.s1 Homo sapiens cDNA clone 276929 3'), R48594 (yj65d07.s1 Homo sapiens cDNA clone 153613 3'), T21160 (Human gene signature HUMGS02466), U43284 (Cloning vector phGFP-S65T, complete sequence, green fluorescent protein (gfp) gene, complete cds), and Z45151 (H. sapiens partial cDNA sequence; clone c-2hh04). The predicted amino acid sequence disclosed herein for AY304\_14 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted AY304\_14 protein demonstrated at least some sequence similarity with sequences identified as D86984 (similar to yeast adenylate cyclase (S56776) [Homo sapiens]), J01415 (cytochrome oxidase subunit 3 [Homo sapiens]), V00662 (cytochrome oxidase III [Homo sapiens]), and X68948 (envelope glycoprotein [Spleen focus-forming virus]). Based upon sequence similarity, AY304\_14 proteins and each homologous protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the AY304\_14 protein sequence, one centered around amino acid 81 and another around amino acid 120 of SEQ ID NO:40.

A polynucleotide of the present invention has been identified as clone "BG160\_1". BG160\_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BG160\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BG160\_1 protein").

The nucleotide sequence of BG160\_1 as presently determined is reported in SEQ ID NO:41, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BG160\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:42. Amino acids 588 to 600 of SEQ ID NO:42 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 601. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the BG160\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BG160\_1 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for BG160\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BG160\_1 demonstrated at least some similarity with sequences identified as A60021 (tropomyosin-related protein, neuronal - rat ;contains element MER27 repetitive element), AA081525 (zn20e02.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone 547994 5'), AA092565 (l15773.seq.F Fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'), D56138 (Human fetal brain cDNA 5'-end GEN-416H11), D61090 (Human fetal brain cDNA 5'-end GEN-155A07), D61184 (Human fetal brain cDNA 5'-end GEN-165A01), L10335 (Homo sapiens neuro-endocrine-specific protein C (NSP) mRNA, complete cds), N21304 (yx53f07.s1 Homo sapiens cDNA clone 265477 3' similar to SP:A60021 A60021 TROPOMYOSIN-RELATED PROTEIN, NEURONAL), and W95814 (ze07f11.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 358317 5' similar to PIR:A60021). The predicted amino acid sequence disclosed herein for BG160\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BG160\_1 protein demonstrated at least some sequence similarity with sequences identified as L10334 (neuroendocrine-specific protein B [Homo sapiens]), L10335 (neuroendocrine-specific protein C [Homo sapiens]). Based upon sequence similarity, BG160\_1 proteins and each homologous protein or peptide may share at least some activity. The TopPredII computer

program predicts three potential transmembrane domains within the BG160\_1 protein sequence, centered around amino acids 84, 484, and 595 of SEQ ID NO:42, respectively.

BG160\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 110 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "BO432\_4"

A polynucleotide of the present invention has been identified as clone "BO432\_4". BO432\_4 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BO432\_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BO432\_4 protein").

The nucleotide sequence of the 5' portion of BO432\_4 as presently determined is reported in SEQ ID NO:43. An additional internal nucleotide sequence from BO432\_4 as presently determined is reported in SEQ ID NO:44. What applicants believe is the proper reading frame and the predicted amino acid sequence encoded by such internal sequence is reported in SEQ ID NO:45. Additional nucleotide sequence from the 3' portion of BO432\_4, including a poly(A) tail, is reported in SEQ ID NO:46.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BO432\_4 should be approximately 1700 bp.

The nucleotide sequence disclosed herein for BO432\_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BO432\_4 demonstrated at least some similarity with sequences identified as AA283626 (zt15e09.s1 Soares NbHTGBC Homo sapiens cDNA clone 713224 3'), AA406486 (zv12g02.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 753458 5' similar to WP F35G2.2 CE05809 E.COLI YCAC LIKE), AA570446 (nk62c12.s1 NCI\_CGAP\_Sch1 Homo sapiens cDNA clone IMAGE:1018102), N55855 (J3389F Homo sapiens cDNA clone J3389 5'), Q10613 (Rianodin receptor gene), T62691 (yc70d10.r1 Homo sapiens cDNA clone 86035 5'), and W90766 (zh79h04.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 418327 3'). The predicted amino acid sequence disclosed herein for BO432\_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BO432\_4 protein demonstrated at least some sequence similarity with sequences identified as Z69637 (F35G2.2 [Caenorhabditis elegans]). Based upon sequence similarity, BO432\_4 proteins and each homologous protein or peptide may share at least some activity. The TopPredII

computer program predicts a potential transmembrane domain at the amino terminus of the BO432\_4 protein sequence. The BO432\_4 protein may also contain the bacterial lysR family signature, a motif found in bacterial transcriptional regulators and which is possibly indicative of a helix-turn-helix structure.

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Clone "BO538\_2"

A polynucleotide of the present invention has been identified as clone "BO538\_2". BO538\_2 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding  
10 a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BO538\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BO538\_2 protein").

The nucleotide sequence of the 5' portion of BO538\_2 as presently determined is reported in SEQ ID NO:47. What applicants presently believe is the proper reading frame for the coding  
15 region is indicated in SEQ ID NO:48. The predicted amino acid sequence of the BO538\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:48. Additional nucleotide sequence from the 3' portion of BO538\_2, including a poly(A) tail, is reported in SEQ ID NO:49.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
20 BO538\_2 should be approximately 3000 bp.

The nucleotide sequence disclosed herein for BO538\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BO538\_2 demonstrated at least some similarity with sequences identified as AA503100 (ne44h01.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA clone 900241), R44035  
25 (yg21g09.s1 Homo sapiens cDNA clone 33167 3'), T21630 (Human gene signature HUMGS03066), and W64854 (me06d12.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 386711 5' similar to PIR S40989 S40989 hypothetical protein F55H2.6 - Caenorhabditis elegans). The predicted amino acid sequence disclosed herein for BO538\_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX  
30 search protocol. The predicted BO538\_2 protein demonstrated at least some sequence similarity with sequences identified as M60525 (nerve growth factor inducible protein [Rattus norvegicus]), R28916 (Type III procollagen), and Z27080 (F55H2.6 [Caenorhabditis elegans]). Based upon sequence similarity, BO538\_2 proteins and each homologous protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains  
35 within the BO538\_2 protein sequence.

Clone "BR595\_4"

A polynucleotide of the present invention has been identified as clone "BR595\_4". BR595\_4 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding  
5 a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BR595\_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BR595\_4 protein").

The nucleotide sequence of the 5' portion of BR595\_4 as presently determined is reported in SEQ ID NO:50. What applicants presently believe is the proper reading frame for the coding  
10 region is indicated in SEQ ID NO:51. The predicted amino acid sequence of the BR595\_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:51. Additional nucleotide sequence from the 3' portion of BR595\_4, including a poly(A) tail, is reported in SEQ ID NO:52.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
15 BR595\_4 should be approximately 3000 bp.

The nucleotide sequence disclosed herein for BR595\_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BR595\_4 demonstrated at least some similarity with sequences identified as AA443742 (zw95b02.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 784683 3'),  
20 AA600820 (np45b08.s1 NCI\_CGAP\_Br1.1 Homo sapiens cDNA clone IMAGE:1129239), T19410 (Human gene signature HUMGS00435), W87465 (zh67c04.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 417126 3'), and Z33587 (H. sapiens partial cDNA sequence; clone HEA89P; single read). Based upon sequence similarity, BR595\_4 proteins and each homologous protein or peptide may share at least some activity.

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Clone "CI490\_2"

A polynucleotide of the present invention has been identified as clone "CI490\_2". CI490\_2 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding  
30 a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CI490\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CI490\_2 protein").

The nucleotide sequence of CI490\_2 as presently determined is reported in SEQ ID NO:53, and includes a poly(A) tail. What applicants presently believe to be the proper reading  
35 frame and the predicted amino acid sequence of the CI490\_2 protein corresponding to the

foregoing nucleotide sequence is reported in SEQ ID NO:54. Amino acids 64 to 76 of SEQ ID NO:54 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 77. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CI490\_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CI490\_2 should be approximately 1200 bp.

The nucleotide sequence disclosed herein for CI490\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CI490\_2 demonstrated at least some similarity with sequences identified as H30751 (yo79a04.r1 Homo sapiens cDNA clone 184110 5'), H49766 (yo24f01.r1 Homo sapiens cDNA clone 178873 5' similar to SP:S19586 N-METHYL-D-ASPARTATE RECEPTOR GLUTAMATE-BINDING CHAIN), H51158 (yo32d04.r1 Homo sapiens cDNA clone 179623 5'), R85211 (yo41d11.s1 Homo sapiens cDNA clone 180501 3' similar to SP S19586 N-METHYL-D-ASPARTATE RECEPTOR GLUTAMATE-BINDING CHAIN), S19586 (N-METHYL-D-ASPARTATE RECEPTOR GLUTAMATE-BINDING CHAIN), S61973 (NMDA receptor glutamate-binding subunit [rat, mRNA]), T01031 (Human leucine zipper protein-kinase cDNA sequence), and W56893 (zc01g05.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 321080 5' similar to PIR S19586 S19586 N-methyl-D-aspartate receptor glutamate-binding chain - rat). The predicted amino acid sequence disclosed herein for CI490\_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CI490\_2 protein demonstrated at least some sequence similarity with sequences identified as S61973 (NMDA receptor glutamate-binding subunit [Rattus sp.]) and U08020 (collagen pro-alpha-1 type I chain [Mus musculus]). Based upon sequence similarity, CI490\_2 proteins and each homologous protein or peptide may share at least some activity. The TopPredII computer program predicts six potential transmembrane domains within the CI490\_2 protein sequence, with the most amino-terminal transmembrane domain centered around amino acid 77 of SEQ ID NO:54.

### 30 Clone "CI522\_1"

A polynucleotide of the present invention has been identified as clone "CI522\_1". CI522\_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence



of the encoded protein. CI522\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CI522\_1 protein").

The nucleotide sequence of the 5' portion of CI522\_1 as presently determined is reported in SEQ ID NO:55. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:56. The predicted amino acid sequence of the CI522\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:56. Amino acids 7 to 19 of SEQ ID NO:56 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CI522\_1 protein. Additional nucleotide sequence from the 3' portion of CI522\_1, including a poly(A) tail, is reported in SEQ ID NO:57.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CI522\_1 should be approximately 1400 bp.

The nucleotide sequence disclosed herein for CI522\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CI522\_1 demonstrated at least some similarity with sequences identified as AA028557 (m18g05.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone 463928 5'), H32238 (EST107136 Rattus sp. cDNA 5' end), T33525 (EST58140 Homo sapiens cDNA 5' end similar to None), U66468 (Human cell growth regulator CGR11 mRNA, complete cds), and X00525 (Mouse 28S ribosomal RNA). The predicted amino acid sequence disclosed herein for CI522\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CI522\_1 protein demonstrated at least some sequence similarity with sequences identified as U66468 (cell growth regulator CGR11 [Homo sapiens]). Based upon sequence similarity, CI522\_1 proteins and each homologous protein or peptide may share at least some activity.

#### Clone "CN238\_1"

A polynucleotide of the present invention has been identified as clone "CN238\_1". CN238\_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CN238\_1 includes at least a portion of the coding sequence of a secreted protein (also referred to herein as "CN238\_1 protein").

The nucleotide sequence of CN238\_1 as presently determined is reported in SEQ ID NO:58, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CN238\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:59.

- 5           The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CN238\_1 should be approximately 2190 bp.

The nucleotide sequence disclosed herein for CN238\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CN238\_1 demonstrated at least some similarity with sequences identified as

10   AA044097 (zk51b02.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 486315 5'),  
AA044287 (zk51b02.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 486315 3'),  
AA045440 (zk67c03.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 487876 3'),  
AA143007 (zl48f01.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 505177 5'),  
D51196 (Human fetal brain cDNA 3'-end GEN-016G05), D60310 (Human fetal brain cDNA  
15   3'-end GEN-098A09), N69344 (yz43e04.s1 Homo sapiens cDNA clone 285822 3' similar to  
gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN)), W22250 (64B8 Human retina cDNA  
Tsp509I-cleaved sublibrary Homo), and X01703 (Human gene for alpha-tubulin (b alpha 1)). The  
predicted amino acid sequence disclosed herein for CN238\_1 was searched against the GenPept  
and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted  
20   CN238\_1 protein demonstrated at least some sequence similarity with sequences identified as  
K00557 (alpha-tubulin [Homo sapiens]) and U51583 (zinc finger homeodomain enhancer-binding  
protein-1 [Rattus norvegicus]). Based upon sequence similarity, CN238\_1 proteins and each  
homologous protein or peptide may share at least some activity.

25           Clone "CO390\_1"

A polynucleotide of the present invention has been identified as clone "CO390\_1". CO390\_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence

30   of the encoded protein. CO390\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CO390\_1 protein").

The nucleotide sequence of CO390\_1 as presently determined is reported in SEQ ID NO:60, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CO390\_1 protein corresponding to the

35   foregoing nucleotide sequence is reported in SEQ ID NO:61.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CO390\_1 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for CO390\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CO390\_1 demonstrated at least some similarity with sequences identified as H84353 (yv85a11.r1 Homo sapiens cDNA clone 249500 5'), L35532 (Pan troglodytes Alu repeat region), N80616 (Genomic clone encoding SAP(Phe)), R53922 (yi03h10.s1 Homo sapiens cDNA clone 138211 3' similar to contains Alu repetitive element; contains TAR1 repetitive element), X75335 (H.sapiens Alu insertion in COL3A1 gene), X95882 (R.norvegicus mRNA for ATP ligand gated ion channel), and Y09561 (H.sapiens mRNA for P2X7 receptor). The predicted amino acid sequence disclosed herein for CO390\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CO390\_1 protein demonstrated at least some sequence similarity with sequences identified as U45448 (P2x1 receptor [Homo sapiens]), W04216 (Rat superior cervical ganglion p2x receptor), X83688 (ATP receptor [Homo sapiens]), X95882 (P2X7 gene product [Rattus norvegicus]), and Y09561 (ATP receptor [Homo sapiens]). Based upon sequence similarity, CO390\_1 proteins and each homologous protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the CO390\_1 protein sequence, centered around amino acid 249 of SEQ ID NO:61. The nucleotide sequence of CO390\_1 may contain an Alu repetitive element.

CO390\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 75 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

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#### Clone "AJ20\_2"

A polynucleotide of the present invention has been identified as clone "AJ20\_2". AJ20\_2 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. AJ20\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AJ20\_2 protein").

The nucleotide sequence of the 5' portion of AJ20\_2 as presently determined is reported in SEQ ID NO:62. What applicants presently believe is the proper reading frame for the coding

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region is indicated in SEQ ID NO:63. The predicted amino acid sequence of the AJ20\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:63. Amino acids 8 to 20 of SEQ ID NO:63 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 21. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the AJ20\_2 protein. Additional nucleotide sequence from the 3' portion of AJ20\_2, including a poly(A) tail, is reported in SEQ ID NO:64.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AJ20\_2 should be approximately 850 bp.

The nucleotide sequence disclosed herein for AJ20\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database.

Clone "AR440\_1"

A polynucleotide of the present invention has been identified as clone "AR440\_1". AR440\_1 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. AR440\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AR440\_1 protein").

The partial nucleotide sequence of AR440\_1, including its 3' end and a poly(A) tail, as presently determined is reported in SEQ ID NO:66. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:67. The predicted amino acid sequence of the AR440\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:67. Additional nucleotide sequence from the 5' portion of AR440\_1 is reported in SEQ ID NO:65.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AR440\_1 should be approximately 1400 bp.

The nucleotide sequence disclosed herein for AR440\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database. The nucleotide sequence of AR440\_1 indicates that it may contain an Alu repetitive element.

Clone "AS164\_1"

A polynucleotide of the present invention has been identified as clone "AS164\_1". AS164\_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. AS164\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AS164\_1 protein").

The nucleotide sequence of AS164\_1 as presently determined is reported in SEQ ID NO:68, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the AS164\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:69.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AS164\_1 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for AS164\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. AS164\_1 demonstrated at least some similarity with sequences identified as H24668 (yl40h10.r1 Homo sapiens cDNA clone 160771 5'), N29757 (yw90h10.s1 Homo sapiens cDNA clone 259555 3'), T62184 (yb96d08.r1 Homo sapiens cDNA clone 79023 5'), Z69706 (Human DNA sequence from cosmid COS12 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs, Flanking sequences of 3' alpha globin H), and Z69890 (Human DNA sequence from cosmid RJ14 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs and CpG island). The predicted amino acid sequence disclosed herein for AS164\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted AS164\_1 protein demonstrated at least some similarity to sequences identified as A20359\_1 (ryanodine receptor gene product [Homo sapiens]) and U78866 (putative arginine-aspartate-rich RNA binding protein [Arabidopsis thaliana]). Based upon sequence similarity, AS164\_1 proteins and each similar protein or peptide may share at least some activity. The predicted AS164\_1 protein sequence also contains repeated Asp-Arg RNA-binding motifs.

### 30      Clone "AX8\_1"

A polynucleotide of the present invention has been identified as clone "AX8\_1". AX8\_1 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence

of the encoded protein. AX8\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AX8\_1 protein").

The nucleotide sequence of AX8\_1 as presently determined is reported in SEQ ID NO:70, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the AX8\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:71. Amino acids 106 to 118 of SEQ ID NO:71 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 119. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the AX8\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AX8\_1 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for AX8\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database. The TopPredII computer program predicts three potential transmembrane domains within the AX8\_1 protein sequence, centered around amino acids 111, 144, and 182 of SEQ ID NO:71, respectively.

AX8\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 35 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "BD176\_3"

A polynucleotide of the present invention has been identified as clone "BD176\_3". BD176\_3 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BD176\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BD176\_3 protein").

The nucleotide sequence of the 5' portion of BD176\_3 as presently determined is reported in SEQ ID NO:72. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:73. The predicted amino acid sequence of the BD176\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:73. Amino acids 2 to 14 of SEQ ID NO:73 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 15. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted

leader/signal sequence not be separated from the remainder of the BD176\_3 protein. Additional nucleotide sequence from the 3' portion of BD176\_3, including a poly(A) tail, is reported in SEQ ID NO:74.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
5 BD176\_3 should be approximately 1300 bp.

The nucleotide sequence disclosed herein for BD176\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BD176\_3 demonstrated at least some similarity with sequences identified as AA029679 (ze94g10.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 366690 5'),  
10 D45913 (Mouse NLRR-1 mRNA for leucine-rich-repeat protein, complete cds), R55610 (yg88h08.r1 Homo sapiens cDNA clone 40606 5'), and T07640 (EST05530 Homo sapiens cDNA clone HFBEM16). The predicted amino acid sequence disclosed herein for BD176\_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BD176\_3 protein demonstrated at least some similarity to  
15 sequences identified as D45913 (leucine-rich-repeat protein [Mus musculus]) and M59472 (asparagine-rich antigen Pfa55-6 [Plasmodium falciparum]). Based upon sequence similarity, BD176\_3 proteins and each similar protein or peptide may share at least some activity.

#### Clone "BD339\_1"

20 A polynucleotide of the present invention has been identified as clone "BD339\_1". BD339\_1 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BD339\_1 is a full-length clone, including the entire coding  
25 sequence of a secreted protein (also referred to herein as "BD339\_1 protein").

The nucleotide sequence of BD339\_1 as presently determined is reported in SEQ ID NO:75, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BD339\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:76.

30 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BD339\_1 should be approximately 650 bp.

The nucleotide sequence disclosed herein for BD339\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BD339\_1 demonstrated at least some similarity with sequences identified as H82422  
35 (yu80d08.s1 Homo sapiens cDNA clone 240111 3), N62058 (EST53c05 Homo sapiens cDNA

clone), U21730 Human 5'-nucleotidase (CD73)), W01979 (za30h09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 294113 5'), and W02015 (za32b11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 294237 5'). Based upon sequence similarity, BD339\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three potential transmembrane domains within the BD339\_1 protein sequence, centered around amino acids 14, 46, and 76 of SEQ ID NO:76, respectively.

#### Clone "BD427\_1"

A polynucleotide of the present invention has been identified as clone "BD427\_1". BD427\_1 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BD427\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BD427\_1 protein").

The nucleotide sequence of BD427\_1 as presently determined is reported in SEQ ID NO:77, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BD427\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:78.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BD427\_1 should be approximately 1810 bp.

The nucleotide sequence disclosed herein for BD427\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BD427\_1 demonstrated at least some similarity with sequences identified as BD427\_1 demonstrated at least some similarity with sequences identified as AA027122 (zk04a03.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 469516 5'), N24735 (yx56b02.s1 Homo sapiens cDNA clone 265707 3'), and W84644 (zd91a06.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 356818 5'). Based upon sequence similarity, BD427\_1 proteins and each similar protein or peptide may share at least some activity.

#### Clone "BL229\_22"

A polynucleotide of the present invention has been identified as clone "BL229\_22". BL229\_22 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino



acid sequence of the encoded protein. BL229\_22 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BL229\_22 protein").

The nucleotide sequence of the 5' portion of BL229\_22 as presently determined is reported in SEQ ID NO:79. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:80. The predicted amino acid sequence of the BL229\_22 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:80. Additional nucleotide sequence from the 3' portion of BL229\_22, including a poly(A) tail, is reported in SEQ ID NO:81.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BL229\_22 should be approximately 870 bp.

The nucleotide sequence disclosed herein for BL229\_22 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database.

Clone "BV123\_16"

A polynucleotide of the present invention has been identified as clone "BV123\_16". BV123\_16 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BV123\_16 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BV123\_16 protein").

The nucleotide sequence of BV123\_16 as presently determined is reported in SEQ ID NO:82, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BV123\_16 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:83.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BV123\_16 should be approximately 1080 bp.

The nucleotide sequence disclosed herein for BV123\_16 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BV123\_16 demonstrated at least some similarity with sequences identified as H29610 (ym61e03.s1 Homo sapiens cDNA clone 52653 3'), H52374 (yq81b12.r1 Homo sapiens cDNA clone 202175 5'), H66213 (yu16h10.s1 Homo sapiens cDNA), L08092 (Homo sapiens dystrophin (DMD) gene, intron 7, transposon-like sequence), L35670 (Homo sapiens (subclone H8 10\_g5 from P1 35 H5 C8) DNA sequence), M62716 (Human CSP-B gene flanking sequence), N46985 (yy83a05.s1 Homo sapiens cDNA clone 280112 3'), R94603 (yq38a04.s1 Homo sapiens

cDNA clone 198030 3'), U91321 (Human chromosome 16p13 BAC clone CIT987SK-363E6, complete sequence), and Z82200 (Human DNA sequence from clone J333E231). Based upon sequence similarity, BV123\_16 proteins and each similar protein or peptide may share at least some activity.

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#### Clone "CH377\_1"

A polynucleotide of the present invention has been identified as clone "CH377\_1". CH377\_1 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CH377\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CH377\_1 protein").

The nucleotide sequence of CH377\_1 as presently determined is reported in SEQ ID NO:84, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CH377\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:85. Amino acids 5 to 17 of SEQ ID NO:85 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CH377\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CH377\_1 should be approximately 570 bp.

The nucleotide sequence disclosed herein for CH377\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CH377\_1 demonstrated at least some similarity with sequences identified as AA507382 (nh73b01.s1 NCI\_CGAP\_Br1.1 Homo sapiens cDNA clone IMAGE 964105) and N70479 (za74f12.s1 Homo sapiens cDNA clone 298319 3'). Based upon sequence similarity, CH377\_1 proteins and each similar protein or peptide may share at least some activity.

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#### Clone "BD441\_1"

A polynucleotide of the present invention has been identified as clone "BD441\_1". BD441\_1 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino

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acid sequence of the encoded protein. BD441\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BD441\_1 protein").

The nucleotide sequence of the 5' portion of BD441\_1 as presently determined is reported in SEQ ID NO:86. An additional internal nucleotide sequence from BD441\_1 as presently  
5 determined is reported in SEQ ID NO:87. What applicants believe is the proper reading frame and the predicted amino acid sequence encoded by such internal sequence is reported in SEQ ID NO:88. Additional nucleotide sequence from the 3' portion of BD441\_1, including a poly(A) tail, is reported in SEQ ID NO:89.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
10 BD441\_1 should be approximately 2400 bp.

The predicted amino acid sequence disclosed herein for BD441\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BD441\_1 protein demonstrated at least some similarity to sequences identified as X61615 (leukemia inhibitory factor receptor [Homo sapiens]). Based upon sequence similarity,  
15 BD441\_1 proteins and each similar protein or peptide may share at least some activity.

#### Clone "BD441\_2"

A polynucleotide of the present invention has been identified as clone "BD441\_2". BD441\_2 was isolated from a human fetal kidney cDNA library using methods which are  
20 selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BD441\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BD441\_2 protein").

The nucleotide sequence of the 5' portion of BD441\_2 as presently determined is reported  
25 in SEQ ID NO:90. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:91. The predicted amino acid sequence of the BD441\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:91. Additional nucleotide sequence from the 3' portion of BD441\_2, including a poly(A) tail, is reported in SEQ ID NO:92.

30 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BD441\_2 should be approximately 1200 bp.

The predicted amino acid sequence disclosed herein for BD441\_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BD441\_2 protein demonstrated at least some similarity to sequences identified as

X61615 (leukemia inhibitory factor receptor [Homo sapiens]). Based upon sequence similarity, BD441\_2 proteins and each similar protein or peptide may share at least some activity.

Clone "BG102\_3"

5 A polynucleotide of the present invention has been identified as clone "BG102\_3". BG102\_3 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BG102\_3 is a full-length clone, including the entire coding sequence of  
10 a secreted protein (also referred to herein as "BG102\_3 protein").

The nucleotide sequence of BG102\_3 as presently determined is reported in SEQ ID NO:93, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BG102\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:94. Amino acids 11 to 23 of SEQ ID  
15 NO:94 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 24. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the BG102\_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
20 BG102\_3 should be approximately 1100 bp.

The nucleotide sequence disclosed herein for BG102\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BG102\_3 demonstrated at least some similarity with sequences identified as AC002078 (Human BAC clone RG111H14 from 7q22, complete sequence), L11910 (Human  
25 retinoblastoma susceptibility gene exons 1-27, complete cds), U62317 (Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence), Z54147 (Human DNA sequence from cosmid L129H7, Huntington's Disease Region, chromosome 4p16.3 contains CpG island), Z75747 (Human DNA sequence from cosmid U96H1, between markers DXS366 and DXS87 on chromosome X \*), and Z80899 (Human DNA sequence from cosmid F1121 on chromosome 6).

30 The predicted amino acid sequence disclosed herein for BG102\_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BG102\_3 protein demonstrated at least some similarity to sequences identified as M13100 (unknown protein [Rattus norvegicus]) and U15647 (reverse transcriptase [Mus musculus]). Based upon sequence similarity, BG102\_3 proteins and each similar protein or

peptide may share at least some activity. The nucleotide sequence of BG102\_3 indicates that it may contain an L1 repetitive element.

BG102\_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 55 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

#### Clone "BK158\_1"

A polynucleotide of the present invention has been identified as clone "BK158\_1". BK158\_1 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BK158\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BK158\_1 protein").

The nucleotide sequence of BK158\_1 as presently determined is reported in SEQ ID NO:95, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BK158\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:96.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BK158\_1 should be approximately 1150 bp.

The nucleotide sequence disclosed herein for BK158\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BK158\_1 demonstrated at least some similarity with sequences identified as N39195 (yv26e08.s1 Homo sapiens cDNA clone 243878 3') and N45263 (yv26e08.r1 Homo sapiens cDNA clone 243878 5'). Based upon sequence similarity, BK158\_1 proteins and each similar protein or peptide may share at least some activity.

BK158\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 28 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "BP163\_1"

A polynucleotide of the present invention has been identified as clone "BP163\_1". BP163\_1 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence

of the encoded protein. BP163\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BP163\_1 protein").

The nucleotide sequence of the 5' portion of BP163\_1 as presently determined is reported in SEQ ID NO:97. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:98. The predicted amino acid sequence of the BP163\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:98. Additional nucleotide sequence from the 3' portion of BP163\_1, including a poly(A) tail, is reported in SEQ ID NO:99.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BP163\_1 should be approximately 1240 bp.

The nucleotide sequence disclosed herein for BP163\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BP163\_1 demonstrated at least some similarity with sequences identified as AA187086 (zp58h06.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone 624443 5' similar to TR G285943 G285943 ORF, COMPLETE CDS), AA301506 (EST14475 Testis tumor Homo sapiens cDNA 5' end similar to hypothetical protein (GB D14659)), D14659 (Human mRNA for KIAA0103 gene, complete cds), and W57328 (ma26d10.r1 Life Tech mouse brain Mus musculus cDNA clone). The predicted amino acid sequence disclosed herein for BP163\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BP163\_1 protein demonstrated at least some similarity to sequences identified as D14659 (KIAA0103 [Homo sapiens]). Based upon sequence similarity, BP163\_1 proteins and each similar protein or peptide may share at least some activity.

#### Clone "BZ16\_3"

A polynucleotide of the present invention has been identified as clone "BZ16\_3". BZ16\_3 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BZ16\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BZ16\_3 protein").

The partial nucleotide sequence of BZ16\_3, including its 3' end and a poly(A) tail, as presently determined is reported in SEQ ID NO:101. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:102. The predicted amino acid sequence of the BZ16\_3 protein corresponding to the foregoing nucleotide sequence is

reported in SEQ ID NO:102. Additional nucleotide sequence from the 5' portion of BZ16\_3 is reported in SEQ ID NO:100.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BZ16\_3 should be approximately 2120 bp.

5       The nucleotide sequence disclosed herein for BZ16\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BZ16\_3 demonstrated at least some similarity with sequences identified as F06886 (H. sapiens partial cDNA sequence; clone c-1nf02), F06870 (H. sapiens partial cDNA sequence; clone c-1nc11), N53511 (yz26b08.s1 Homo sapiens cDNA clone 284151 3'), T65313 (yc79g12.s1  
10 Homo sapiens cDNA clone 22132 3'), U00084 (Haemophilus influenzae), W44815 (zc21d01.s1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 322945 3'), and Z49128 (Caenorhabditis elegans cosmid M03C11). The predicted amino acid sequence disclosed herein for BZ16\_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BZ16\_3 protein demonstrated at least some  
15 similarity to sequences identified as D26185 (cell division protein [Bacillus subtilis]), L46096 (HEAH1465\_1 cell division protein [Haemophilus influenzae]), and Z49128 (CEM03C11\_5 M03C11.5 [Caenorhabditis elegans]). The BZ16\_3 protein demonstrated at least some similarity to ATP-dependent proteases such as ftsH. Based upon sequence similarity, BZ16\_3 proteins and each similar protein or peptide may share at least some activity.

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#### Clone "CC182\_1"

A polynucleotide of the present invention has been identified as clone "CC182\_1". CC182\_1 was isolated from a human adult brain cDNA library using methods which are selective  
25 for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CC182\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CC182\_1 protein").

The nucleotide sequence of CC182\_1 as presently determined is reported in SEQ ID  
30 NO:103, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CC182\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:104. Amino acids 26 to 38 of SEQ ID NO:104 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 39. Due to the hydrophobic nature of the predicted leader/signal

sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CC182\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CC182\_1 should be approximately 1600 bp.

5        The nucleotide sequence disclosed herein for CC182\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CC182\_1 demonstrated at least some similarity with sequences identified as H61159 (yu37f08.s1 Homo sapiens cDNA clone 236007 3' similar to contains L1 repetitive element), L09709 (Human lysosomal-associated membrane glycoprotein-2 (LAMP2) gene, 5' end of CDS  
10       and flanking region), W44797 (zb98e10.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 320874 3' similar to contains Alu repetitive element), and X62167 (H.sapiens mRNA for P2 protein of peripheral myelin). Based upon sequence similarity, CC182\_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of CC182\_1 indicates that it may contain an L1 repetitive element and/or a MER42C repetitive element.

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#### Clone "CG109\_1"

A polynucleotide of the present invention has been identified as clone "CG109\_1". CG109\_1 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding  
20       a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CG109\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CG109\_1 protein").

The nucleotide sequence of CG109\_1 as presently determined is reported in SEQ ID NO:105, and includes a poly(A) tail. What applicants presently believe to be the proper reading  
25       frame and the predicted amino acid sequence of the CG109\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:106.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CG109\_1 should be approximately 600 bp.

The nucleotide sequence disclosed herein for CG109\_1 was searched against the GenBank  
30       and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database.

#### Clone "CJ397\_1"

A polynucleotide of the present invention has been identified as clone "CJ397\_1".  
35       CJ397\_1 was isolated from a human fetal brain cDNA library using methods which are selective



for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CJ397\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CJ397\_1 protein").

5       The nucleotide sequence of the 5' portion of CJ397\_1 as presently determined is reported in SEQ ID NO:107. An additional internal nucleotide sequence from CJ397\_1 as presently determined is reported in SEQ ID NO:108. What applicants believe is the proper reading frame and the predicted amino acid sequence encoded by such internal sequence is reported in SEQ ID NO:109. Additional nucleotide sequence from the 3' portion of CJ397\_1, including a poly(A)  
10 tail, is reported in SEQ ID NO:110.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CJ397\_1 should be approximately 1900 bp.

The nucleotide sequence disclosed herein for CJ397\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search  
15 protocols. CJ397\_1 demonstrated at least some similarity with sequences identified as H18685 (yn52b08.s1 Homo sapiens cDNA clone 172023 3'), H46001 (yo13f06.s1 Homo sapiens cDNA clone 177827 3'), and T77612 (yc91f06.r1 Homo sapiens cDNA clone 23298 5'). Based upon sequence similarity, CJ397\_1 proteins and each similar protein or peptide may share at least some activity.

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#### Clone "AM795\_4"

A polynucleotide of the present invention has been identified as clone "AM795\_4". AM795\_4 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified  
25 as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. AM795\_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AM795\_4 protein").

The nucleotide sequence of AM795\_4 as presently determined is reported in SEQ ID NO:111, and includes a poly(A) tail. What applicants presently believe to be the proper reading  
30 frame and the predicted amino acid sequence of the AM795\_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:112. Amino acids 9 to 21 of SEQ ID NO:112 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 22. Amino acids 138 to 150 of SEQ ID NO:112 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid  
35 151. Due to the hydrophobic nature of the predicted and the possible leader/signal sequences,

each of such sequences may act as a transmembrane domain should that leader/signal sequence not be separated from the remainder of the AM795\_4 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AM795\_4 should be approximately 1900 bp.

5       The nucleotide sequence disclosed herein for AM795\_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. AM795\_4 demonstrated at least some similarity with sequences identified as AF002700 (Homo sapiens GDNF family receptor alpha 2 (GFRalpha2) mRNA, complete cds), H05619 (y170a10.s1 Homo sapiens cDNA clone 43207 3'), U46493 (Cloning vector pFlp recombina

10       se gene, complete cds), U59486 (Rattus norvegicus GDNF receptor alpha mRNA, complete cds), V00248 (Human Ret ligand retL2 cDNA), W73633 (zd55h01.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 344593 3', mRNA sequence), and W73681 (zd55h01.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 344593 5', mRNA sequence). The predicted amino acid sequence disclosed herein for AM795\_4 was searched against the GenPept

15       and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted AM795\_4 protein demonstrated at least some similarity to sequences identified as AF002700 (GDNF family receptor alpha 2 (GFRalpha2) [Homo sapiens]), U59486 (GDNF receptor alpha [Rattus norvegicus]), and W37460 (Human Ret ligand retL2 cDNA). A receptor complex comprised of TrnR1 (GDNFR alpha) and Ret was found to be capable of mediating both GDNF

20       and NTN signaling. The receptor called TrnR2, identified based on homology to TrnR1, is 48% identical to TrnR1 and is encoded by a gene located on the short arm of chromosome 8. TrnR2 is attached to the cell surface via a GPI-linkage, and can mediate both NTN and GDNF signaling through Ret *in vitro* (Baloh *et al.*, 1997, *Neuron* 18(5): 793-802, which is incorporated by reference herein). Based upon sequence similarity, AM795\_4 proteins and each similar protein

25       or peptide may share at least some activity.

AM795\_4 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 76 kDa was detected in conditioned media fractions using SDS polyacrylamide gel electrophoresis.

### 30       Clone "AT340\_1"

A polynucleotide of the present invention has been identified as clone "AT340\_1". AT340\_1 was isolated from a human adult blood (lymphocytes and dendritic cells treated with mixed lymphocyte reaction) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or

35       transmembrane protein on the basis of computer analysis of the amino acid sequence of the

encoded protein. AT340\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AT340\_1 protein").

The partial nucleotide sequence of AT340\_1, including its 3' end and a poly(A) tail, as presently determined is reported in SEQ ID NO:114. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:115. The predicted amino acid sequence of the AT340\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:115. Amino acids 12 to 24 of SEQ ID NO:115 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 25. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the AT340\_1 protein. Additional nucleotide sequence from the 5' portion of AT340\_1 is reported in SEQ ID NO:113.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AT340\_1 should be approximately 1100 bp.

The nucleotide sequence disclosed herein for AT340\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. AT340\_1 demonstrated at least some similarity with sequences identified as AA039343 (zk39g04.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 485238 3'), R68951 (yi43g06.r1 Homo sapiens cDNA clone 142042 5' similar to SP:C35D10.1 CE01190), R77532 (yi76c01.r1 Homo sapiens cDNA), R92619 (yq04a04.r1 Homo sapiens cDNA clone 195918 5' similar to SP:C35D10.1 CE01190), and W60997 (zc99f09.s1 Pancreatic Islet Homo sapiens cDNA clone 339305 3'). The predicted amino acid sequence disclosed herein for AT340\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted AT340\_1 protein demonstrated at least some similarity to sequences identified as U21324 (similar to *S. cerevisiae* hypothetical protein YKL166 [*Caenorhabditis elegans*]). Based upon sequence similarity, AT340\_1 proteins and each similar protein or peptide may share at least some activity.

#### Clone "BG132\_1"

A polynucleotide of the present invention has been identified as clone "BG132\_1". BG132\_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BG132\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BG132\_1 protein").

The nucleotide sequence of the 5' portion of BG132\_1 as presently determined is reported in SEQ ID NO:116. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:117. The predicted amino acid sequence of the BG132\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:117.

- 5 Amino acids 121 to 133 of SEQ ID NO:117 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 134. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the BG132\_1 protein. Additional nucleotide sequence from the 3' portion of BG132\_1, including a poly(A) tail,  
10 is reported in SEQ ID NO:118.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BG132\_1 should be approximately 2000 bp.

- The nucleotide sequence disclosed herein for BG132\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search  
15 protocols. BG132\_1 demonstrated at least some similarity with sequences identified as AA078587 (7P05H12 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P05H12), H14301 (ym63c04.r1 Homo sapiens cDNA clone 163590 5' similar to gb:U03642\_cds1 PROBABLE G PROTEIN-COUPLED RECEPTOR APJ (HUMAN)), L09249 (putative G-protein coupled receptor, rhodopsin family), S79811 (adrenomedullin receptor [rats,  
20 lung, mRNA]), T36034 (rchd523 gene differentially expressed in cardiovascular disease), U58828 (Human IL8-related receptor (DRY12) mRNA, complete cds), and Y08162 (H.sapiens mRNA for heptahelix receptor). The predicted amino acid sequence disclosed herein for BG132\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BG132\_1 protein demonstrated at least some similarity to  
25 sequences identified as L06109 (G protein-coupled receptor [Gallus gallus]), L34339 (galanin receptor [Homo sapiens]), U30290 (galanin receptor GALR1 [Rattus norvegicus]), U58828 (IL8-related receptor [Homo sapiens]), W03739 (rchd523 gene product (G protein-coupled receptor)), X98510 (G protein-coupled receptor [Homo sapiens]), and Y08162 (heptahelix receptor [Homo sapiens]). Based upon sequence similarity, BG132\_1 proteins and each similar  
30 protein or peptide may share at least some activity.

#### Clone "BG219\_2"

- A polynucleotide of the present invention has been identified as clone "BG219\_2". BG219\_2 was isolated from a human adult brain cDNA library using methods which are selective  
35 for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding

a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BG219\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BG219\_2 protein").

5 The nucleotide sequence of BG219\_2 as presently determined is reported in SEQ ID NO:119, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BG219\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:120.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BG219\_2 should be approximately 700 bp.

10 The nucleotide sequence disclosed herein for BG219\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BG219\_2 demonstrated at least some similarity with sequences identified as AA210695 (zr88b05.s1 Soares NbHTGBC Homo sapiens cDNA clone 682737 3'), C01459 (HUMGS0008450, Human Gene Signature, 3'-directed cDNA sequence), N22628 (EST49p115  
15 Homo sapiens cDNA clone 49p115), and T26211 (Human gene signature HUMGS08450). Based upon sequence similarity, BG219\_2 proteins and each similar protein or peptide may share at least some activity.

#### Clone "BG366\_2"

20 A polynucleotide of the present invention has been identified as clone "BG366\_2". BG366\_2 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BG366\_2 is a full-length clone, including the entire coding sequence of  
25 a secreted protein (also referred to herein as "BG366\_2 protein").

The nucleotide sequence of BG366\_2 as presently determined is reported in SEQ ID NO:121, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BG366\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:122. The amino acid sequence of  
30 another protein that could be encoded by BG366\_2 is reported in SEQ ID NO:283.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BG366\_2 should be approximately 3000 bp.

The nucleotide sequence disclosed herein for BG366\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search  
35 protocols. BG366\_2 demonstrated at least some similarity with sequences identified as N39453

(yy49h03.s1 Homo sapiens cDNA clone 276917 3'). Based upon sequence similarity, BG366\_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the BG366\_2 protein sequence centered around amino acid 92 of SEQ ID NO:122.

5

#### Clone "BV172\_2"

A polynucleotide of the present invention has been identified as clone "BV172\_2". BV172\_2 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding  
10 a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BV172\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BV172\_2 protein").

The nucleotide sequence of BV172\_2 as presently determined is reported in SEQ ID NO:123, and includes a poly(A) tail. What applicants presently believe to be the proper reading  
15 frame and the predicted amino acid sequence of the BV172\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:124.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BV172\_2 should be approximately 1650 bp.

The nucleotide sequence disclosed herein for BV172\_2 was searched against the GenBank  
20 and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BV172\_2 demonstrated at least some similarity with sequences identified as No significant hits were found in the database. The TopPredII computer program predicts a potential transmembrane domain within the BV172\_2 protein sequence centered around amino acid 19 of SEQ ID NO:124. The nucleotide sequence of BV172\_2 indicates that it may contain one or more  
25 of the following types of repetitive elements: an element similar to chicken CR1, human L1, Mer33.

30

#### Clone "CC247\_10"

A polynucleotide of the present invention has been identified as clone "CC247\_10". CC247\_10 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino

acid sequence of the encoded protein. CC247\_10 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CC247\_10 protein").

The nucleotide sequence of CC247\_10 as presently determined is reported in SEQ ID NO:125, and includes a poly(A) tail. What applicants presently believe to be the proper reading  
5 frame and the predicted amino acid sequence of the CC247\_10 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:126. Amino acids 1 to 8 of SEQ ID NO:126 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 9. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be  
10 separated from the remainder of the CC247\_10 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CC247\_10 should be approximately 550 bp.

The nucleotide sequence disclosed herein for CC247\_10 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA  
15 search protocols. CC247\_10 demonstrated at least some similarity with sequences identified as AA291226 (zs47d03.r1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone 700613 5'), T05738 (EST03627 Homo sapiens cDNA clone HFBDF64), W51195 (ma14b04.r1 Life Tech mouse brain Mus musculus cDNA clone 304495 5'), and W93640 (zd95d09.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 357233 3'). The predicted amino acid sequence disclosed herein for  
20 CC247\_10 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CC247\_10 protein demonstrated at least some similarity to sequences identified as M62424 (thrombin receptor [Homo sapiens]). The predicted CC247\_10 protein is highly hydrophobic. Based upon sequence similarity, CC247\_10 proteins and each similar protein or peptide may share at least some activity.

25

#### Clone "CI480\_9"

A polynucleotide of the present invention has been identified as clone "CI480\_9". CI480\_9 was isolated from a human adult brain cDNA library using methods which are selective  
30 for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CI480\_9 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CI480\_9 protein").

The nucleotide sequence of CI480\_9 as presently determined is reported in SEQ ID  
35 NO:127, and includes a poly(A) tail. What applicants presently believe to be the proper reading

frame and the predicted amino acid sequence of the CI480\_9 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:128. Amino acids 39 to 51 of SEQ ID NO:128 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 52. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CI480\_9 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CI480\_9 should be approximately 1940 bp.

The nucleotide sequence disclosed herein for CI480\_9 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CI480\_9 demonstrated at least some similarity with sequences identified as N99342 (IMAGE:20093 Homo sapiens cDNA clone 20093), R89725 (ym99d09.r1 Homo sapiens cDNA clone 167057 5'), and U60644 (Human HU-K4 mRNA, complete cds). The predicted amino acid sequence disclosed herein for CI480\_9 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CI480\_9 protein demonstrated at least some similarity to sequences identified as U60644 (HU-K4 [Homo sapiens]). Based upon sequence similarity, CI480\_9 proteins and each similar protein or peptide may share at least some activity.

CI480\_9 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 63 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "CO722\_1"

A polynucleotide of the present invention has been identified as clone "CO722\_1". CO722\_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CO722\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CO722\_1 protein").

The nucleotide sequence of CO722\_1 as presently determined is reported in SEQ ID NO:129, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CO722\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:130. Amino acids 17 to 29 of SEQ ID NO:130 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 30. Due to the hydrophobic nature of the predicted leader/signal



sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CO722\_1 protein.

The EcoRI/NtI restriction fragment obtainable from the deposit containing clone CO722\_1 should be approximately 6800 bp.

5       The nucleotide sequence disclosed herein for CO722\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CO722\_1 demonstrated at least some similarity with sequences identified as AA186616 (zp71a08.s1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone 625622 3' similar to contains Alu repetitive element), H10376 (ym08a03.s1 Homo sapiens cDNA clone 10 47067 3'), N86013 (J5997F Fetal heart, Lambda ZAP Express Homo sapiens cDNA), U55258 (Human hBRAVO/Nr-CAM precursor (hBRAVO/ Nr-CAM) gene, complete cds), W19770 (zb39d01.r1 Soares parathyroid tumor NbHPA Homo sapiens), W31608 (zb91d09.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone), and X58482 (Chicken mRNA for neuronal transmembrane protein Nr-CAM, ng-CAM related). The predicted amino acid sequence 15 disclosed herein for CO722\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CO722\_1 protein demonstrated at least some similarity to sequences identified as AB002341 (KIAA0343 [Homo sapiens]) and X58482 (Nr-CAM protein [Gallus gallus]). Based upon sequence similarity, CO722\_1 proteins and each similar protein or peptide may share at least some activity. The 20 TopPredII computer program predicts two potential transmembrane domains within the CO722\_1 protein sequence, centered around amino acids 610 and 1070 of SEQ ID NO:130, respectively.

CO722\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 160 kDa was detected in conditioned media fractions using SDS polyacrylamide gel electrophoresis.

25

#### Clone "CT748\_2"

A polynucleotide of the present invention has been identified as clone "CT748\_2". CT748\_2 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding 30 a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CT748\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CT748\_2 protein").

The nucleotide sequence of CT748\_2 as presently determined is reported in SEQ ID NO:131, and includes a poly(A) tail. What applicants presently believe to be the proper reading 35 frame and the predicted amino acid sequence of the CT748\_2 protein corresponding to the

foregoing nucleotide sequence is reported in SEQ ID NO:132. Amino acids 281 to 293 of SEQ ID NO:132 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 294. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CT748\_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CT748\_2 should be approximately 5500 bp.

The nucleotide sequence disclosed herein for CT748\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CT748\_2 demonstrated at least some similarity with sequences identified as T48063 (yb24f03.s1 Homo sapiens cDNA clone 72125 3') and X54175 (Human specific Alu element (HS C4N2) DNA). The predicted amino acid sequence disclosed herein for CT748\_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CT748\_2 protein demonstrated at least some similarity to sequences identified as Z36714 (cyclin F [Homo sapiens]). Based upon sequence similarity, CT748\_2 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of CT748\_2 indicates that it may contain an Alu repetitive element.

#### Clone "AJ1\_1"

A polynucleotide of the present invention has been identified as clone "AJ1\_1". AJ1\_1 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. AJ1\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AJ1\_1 protein").

The nucleotide sequence of the 5' portion of AJ1\_1 as presently determined is reported in SEQ ID NO:133. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:134. The predicted amino acid sequence of the AJ1\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:134. Additional nucleotide sequence from the 3' portion of AJ1\_1, including a poly(A) tail, is reported in SEQ ID NO:135.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AJ1\_1 should be approximately 925 bp.

The predicted amino acid sequence disclosed herein for AJ1\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The

predicted AJ1\_1 protein demonstrated at least some similarity to sequences identified as U39060 (GRIP1 [Mus musculus]). Based upon sequence similarity, AJ1\_1 proteins and each similar protein or peptide may share at least some activity.

5        Clone "AQ73\_3"

A polynucleotide of the present invention has been identified as clone "AQ73\_3". AQ73\_3 was isolated from a human adult ovary (PA-1 teratocarcinoma, untreated tissue pooled with retinoic-acid-treated and activin-treated tissue) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified  
10 as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. AQ73\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AQ73\_3 protein").

The nucleotide sequence of AQ73\_3 as presently determined is reported in SEQ ID NO:136, and includes a poly(A) tail. What applicants presently believe to be the proper reading  
15 frame and the predicted amino acid sequence of the AQ73\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:137.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AQ73\_3 should be approximately 2800 bp.

The nucleotide sequence disclosed herein for AQ73\_3 was searched against the GenBank  
20 and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. AQ73\_3 demonstrated at least some similarity with sequences identified as AA514474 (nf57g01.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA clone 924048), T47520 (Human hepatoma-derived growth factor (HDGF-2) cDNA), W24708 (zb62e08.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 308198 5'), and W45513 (zc27g08.s1 Soares senescent  
25 fibroblasts NbHSF Homo sapiens cDNA clone 323582 3'). The predicted amino acid sequence disclosed herein for AQ73\_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted AQ73\_3 protein demonstrated at least some similarity to sequences identified as D16431 (hepatoma-derived GF [Homo sapiens]), D63707 (mouse hepatoma derived growth factor (HDGF) [Mus musculus]), R66727 (Human  
30 hepatoma derived growth factor), U18997 (ORF\_f299 [Escherichia coli]), U97193 (similar to S. cerevisiae SIR2 (SP P06700) and mouse hepatoma derived growth factor HDGF (NID g945418) [Caenorhabditis elegans]), and W09404 (Human hepatoma-derived growth factor (HDGF-2)). Based upon sequence similarity, AQ73\_3 proteins and each similar protein or peptide may share at least some activity.

AQ73\_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 67 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

5           Clone "BG142\_1"

A polynucleotide of the present invention has been identified as clone "BG142\_1". BG142\_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence  
10 of the encoded protein. BG142\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BG142\_1 protein").

The nucleotide sequence of BG142\_1 as presently determined is reported in SEQ ID NO:138, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BG142\_1 protein corresponding to the  
15 foregoing nucleotide sequence is reported in SEQ ID NO:139.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BG142\_1 should be approximately 1100 bp.

The nucleotide sequence disclosed herein for BG142\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search  
20 protocols. BG142\_1 demonstrated at least some similarity with sequences identified as AA170261 (ms87h11.r1 Soares mouse 3NbMS Mus musculus cDNA clone 618597 5' similar to TR E245601 E245601 G-RICH BOX-BINDING PROTEIN), L04282 (Human CACCC box-binding protein mRNA, complete cds), N27696 (yx51h12.r1 Homo sapiens cDNA clone 265319 5'), W96110 (ze09a11.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone  
25 358460 5'), and W96111 (ze09a11.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 358460 3'). The predicted amino acid sequence disclosed herein for BG142\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BG142\_1 protein demonstrated at least some similarity to sequences identified as U80078 (transcription factor BFCOL1 [Mus musculus]) and X98096 (G-rich  
30 box-binding protein [Mus musculus]). Based upon sequence similarity, BG142\_1 proteins and each similar protein or peptide may share at least some activity.

Clone "BV66\_1"

A polynucleotide of the present invention has been identified as clone "BV66\_1".  
35 BV66\_1 was isolated from a human adult brain cDNA library using methods which are selective

for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BV66\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BV66\_1 protein").

5       The nucleotide sequence of BV66\_1 as presently determined is reported in SEQ ID NO:140, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BV66\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:141.

10       The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BV66\_1 should be approximately 870 bp.

      The nucleotide sequence disclosed herein for BV66\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database. The nucleotide sequence of BV66\_1 indicates that it may contain a TAAA1 simple repeat element.

15

#### Clone "BV291\_3"

      A polynucleotide of the present invention has been identified as clone "BV291\_3". BV291\_3 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding  
20   a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BV291\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BV291\_3 protein").

      The nucleotide sequence of BV291\_3 as presently determined is reported in SEQ ID NO:142, and includes a poly(A) tail. What applicants presently believe to be the proper reading  
25   frame and the predicted amino acid sequence of the BV291\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:143.

      The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BV291\_3 should be approximately 2000 bp.

      The nucleotide sequence disclosed herein for BV291\_3 was searched against the GenBank  
30   and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BV291\_3 demonstrated at least some similarity with sequences identified as H10954 (ym06e09.r1 Homo sapiens cDNA clone 47034 5'), H10955 (ym06e09.s1 Homo sapiens cDNA clone 47034 3'), N25300 (yw52c10.s1 Homo sapiens cDNA clone 255858 3'), T25940 (Human gene signature HUMGS08173), T68890 (yc30g11.s1 Homo sapiens cDNA clone 82244 3'),  
35   T78286 (yc99a08.r1 Homo sapiens cDNA clone 24033 5'), Z39987 (H. sapiens partial cDNA

sequence; clone c-1oh05), and Z47073 (Caenorhabditis elegans cosmid ZC506). The predicted amino acid sequence disclosed herein for BV291\_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BV291\_3 protein demonstrated at least some similarity to sequences identified as X02155  
5 (BTTGR\_1 thyroglobulin [Bos taurus]). Based upon sequence similarity, BV291\_3 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the BV291\_3 protein sequence centered around amino acid 48 of SEQ ID NO:143.

BV291\_3 protein was expressed in a COS cell expression system, and an expressed protein  
10 band of approximately 30 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

#### Clone "CK201\_1"

A polynucleotide of the present invention has been identified as clone "CK201\_1".  
15 CK201\_1 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CK201\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CK201\_1 protein").

20 The nucleotide sequence of CK201\_1 as presently determined is reported in SEQ ID NO:144, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CK201\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:145.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
25 CK201\_1 should be approximately 1080 bp.

The nucleotide sequence disclosed herein for CK201\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CK201\_1 demonstrated at least some similarity with sequences identified as AA129133 (zo09h12.s1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA  
30 clone 567239 3' similar to contains Alu repetitive element), D81444 (Human fetal brain cDNA 5'-end GEN-164G10), R36326 (yg69h09.r1 Homo sapiens cDNA clone 38821 5'), T08553 (Oncogene R-ras mutant cDNA (exons 2-6)), T31595 (Probe (BLUR13) for Alu repeat sequence), X03273 (Human Alu-family cluster 5' of alpha(1)-acid glycoprotein gene), and X69907 (H.sapiens gene for mitochondrial ATP synthase c subunit). The predicted amino acid sequence  
35 disclosed herein for CK201\_1 was searched against the GenPept and GeneSeq amino acid

sequence databases using the BLASTX search protocol. The predicted CK201\_1 protein demonstrated at least some similarity to sequences identified as D21827 (major surface glycoprotein [*Pneumocystis carinii*]). Based upon sequence similarity, CK201\_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of  
5 CK201\_1 indicates that it may contain an Alu repetitive element.

CK201\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 40 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

10 Clone "CQ331\_2"

A polynucleotide of the present invention has been identified as clone "CQ331\_2". CQ331\_2 was isolated from a human adult heart cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence  
15 of the encoded protein. CQ331\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CQ331\_2 protein").

The nucleotide sequence of CQ331\_2 as presently determined is reported in SEQ ID NO:146, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CQ331\_2 protein corresponding to the  
20 foregoing nucleotide sequence is reported in SEQ ID NO:147. Amino acids 7 to 19 of SEQ ID NO:147 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CQ331\_2 protein.

25 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CQ331\_2 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for CQ331\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CQ331\_2 demonstrated at least some similarity with sequences identified as J03766  
30 (Canine cardiac calsequestrin mRNA, complete cds), L29766 (*Homo sapiens* epoxide hydrolase (EPHX) gene, complete cds), N83601 (KK1173F *Homo sapiens* cDNA clone KK1173 5' similar to CALSEQUESTRIN (CARDIAC)), T99646 (ye73f12.s1 *Homo sapiens* cDNA clone 123407 3' similar t contains Alu repetitive element;contains PTR5 repetitive element), and W76326 (zd60d04.r1 Soares fetal heart NbHH19W *Homo sapiens* cDNA clone 345031 5' similar to  
35 contains Alu repetitive element). The predicted amino acid sequence disclosed herein for

CQ331\_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CQ331\_2 protein demonstrated at least some similarity to sequences identified as J03766 (DOGCAL\_1 Canine cardiac calsequestrin mRNA, complete cds [Canis canis]) and X55040 (calsequestrin [Oryctolagus cuniculus]). Based upon  
5 sequence similarity, CQ331\_2 proteins and each similar protein or peptide may share at least some activity.

#### Clone "CT550\_1"

A polynucleotide of the present invention has been identified as clone "CT550\_1".  
10 CT550\_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CT550\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CT550\_1 protein").

15 The nucleotide sequence of CT550\_1 as presently determined is reported in SEQ ID NO:148, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CT550\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:149.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
20 CT550\_1 should be approximately 1070 bp.

The nucleotide sequence disclosed herein for CT550\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database. The TopPredII computer program predicts a potential transmembrane domain within the CT550\_1 protein sequence centered around amino  
25 acid 25 of SEQ ID NO:149.

CT550\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 7 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

#### 30 Clone "CT585\_1"

A polynucleotide of the present invention has been identified as clone "CT585\_1". CT585\_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence



of the encoded protein. CT585\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CT585\_1 protein").

The nucleotide sequence of CT585\_1 as presently determined is reported in SEQ ID NO:150, and includes a poly(A) tail. What applicants presently believe to be the proper reading  
5 frame and the predicted amino acid sequence of the CT585\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:151. Amino acids 2 to 14 of SEQ ID NO:151 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 15. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal  
10 sequence not be separated from the remainder of the CT585\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CT585\_1 should be approximately 2710 bp.

The nucleotide sequence disclosed herein for CT585\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search  
15 protocols. CT585\_1 demonstrated at least some similarity with sequences identified as AA069442 (zf74b02.s1 Soares pineal gland N3HPG Homo sapiens cDNA clone 382635 3'), L38961 (Homo sapiens putative transmembrane protein (B5) mRNA, complete cds), N34932 (yy49b10.s1 Homo sapiens cDNA clone 276859 3'), N60101 (TgESTzy11f10.r1 Toxoplasma gondii cDNA clone tgzy11f10.r1 5'), and U13019 (Caenorhabditis elegans cosmid T12A2). The predicted amino acid  
20 sequence disclosed herein for CT585\_1 was searched against the GenPept, GeneSeq, and SwissProt amino acid sequence databases using the BLASTX search protocol. The predicted CT585\_1 protein demonstrated at least some similarity to sequences identified as L34260 (transmembrane protein [Mus musculus]), L38961 (transmembrane protein [Homo sapiens]), P46975 (Caenorhabditis elegans oligosaccharyl transferase stt3 [Caenorhabditis elegans]), and  
25 U13019 (Caenorhabditis elegans cosmid T12A2 [Caenorhabditis elegans]). Based upon sequence similarity, CT585\_1 proteins and each similar protein or peptide may share at least some activity.

#### Clone "CT797\_3"

A polynucleotide of the present invention has been identified as clone "CT797\_3".  
30 CT797\_3 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CT797\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CT797\_3 protein").

The nucleotide sequence of CT797\_3 as presently determined is reported in SEQ ID NO:152, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CT797\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:153.

5           The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CT797\_3 should be approximately 3300 bp.

The nucleotide sequence disclosed herein for CT797\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CT797\_3 demonstrated at least some similarity with sequences identified as AA573847  
10 (nk08d06.s1 NCI\_CGAP\_Co2 Homo sapiens cDNA clone IMAGE:1012907). The predicted amino acid sequence disclosed herein for CT797\_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CT797\_3 protein demonstrated at least some similarity to sequences identified as U18309 (chromokinesin [Gallus gallus]) and Z82271 (T01G1.1 [Caenorhabditis elegans]). Based upon  
15 sequence similarity, CT797\_3 proteins and each similar protein or peptide may share at least some activity.

CT797\_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 80 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

20

#### Clone "CB107\_1"

A polynucleotide of the present invention has been identified as clone "CB107\_1". CB107\_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding  
25 a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CB107\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CB107\_1 protein").

The nucleotide sequence of the 5' portion of CB107\_1 as presently determined is reported in SEQ ID NO:154. An additional internal nucleotide sequence from CB107\_1 as presently  
30 determined is reported in SEQ ID NO:155. What applicants believe is the proper reading frame and the predicted amino acid sequence encoded by such internal sequence is reported in SEQ ID NO:156. Additional nucleotide sequence from the 3' portion of CB107\_1, including a poly(A) tail, is reported in SEQ ID NO:157.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
35 CB107\_1 should be approximately 3300 bp.

The nucleotide sequence disclosed herein for CB107\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CB107\_1 demonstrated at least some similarity with sequences identified as AA121485 (zn80a02.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone 564458 3'),  
5 AA428192 (zw51b08.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773559 3'), D83018 (Human mRNA for nel-related protein 2, complete cds), F10919 (H. sapiens partial cDNA sequence; clone c-3lg01), H15375 (ym28d09.r1 Homo sapiens cDNA clone 49527 5' similar to SP A54105 A54105 FIBRILLIN-2 PRECURSOR), U48245 (Rattus norvegicus protein kinase C-binding protein Nel mRNA, complete cds), U59230 (Mus musculus mel (MEL91)  
10 mRNA, complete cds), and W28387 (46c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA). The predicted amino acid sequence disclosed herein for CB107\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CB107\_1 protein demonstrated at least some similarity to sequences identified as D83018 (nel-related protein 2 [Homo sapiens]), R05222 (Antigen  
15 GX5401FL encoded by Eimeria tenella genomic DNA), R79964 (Connective tissue growth factor), U48245 (RNU48245\_1 protein kinase C-binding protein Nel [Rattus norvegicus]), and U59230 (mel [Mus musculus]). Based upon sequence similarity, CB107\_1 proteins and each similar protein or peptide may share at least some activity.

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#### Clone "CG300\_3"

A polynucleotide of the present invention has been identified as clone "CG300\_3". CG300\_3 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding  
25 a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CG300\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CG300\_3 protein").

The nucleotide sequence of CG300\_3 as presently determined is reported in SEQ ID NO:158, and includes a poly(A) tail. What applicants presently believe to be the proper reading  
30 frame and the predicted amino acid sequence of the CG300\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:159. Amino acids 30 to 42 of SEQ ID NO:159 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 43. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal  
35 sequence not be separated from the remainder of the CG300\_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CG300\_3 should be approximately 1800 bp.

The nucleotide sequence disclosed herein for CG300\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CG300\_3 demonstrated at least some similarity with sequences identified as N40185 (yy44d08.s1 Homo sapiens cDNA clone 276399 3') and W01791 (za72d06.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 298091 5'). Based upon sequence similarity, CG300\_3 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four potential transmembrane domains within the CG300\_3 protein sequence, centered around amino acids 34, 98, 151, and 179 of SEQ ID NO:159, respectively.

CG300\_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 29 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "CJ145\_1"

A polynucleotide of the present invention has been identified as clone "CJ145\_1". CJ145\_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CJ145\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CJ145\_1 protein").

The nucleotide sequence of CJ145\_1 as presently determined is reported in SEQ ID NO:160, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CJ145\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:161. Amino acids 6 to 18 of SEQ ID NO:161 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 19. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CJ145\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CJ145\_1 should be approximately 3600 bp.

The nucleotide sequence disclosed herein for CJ145\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search

protocols. CJ145\_1 demonstrated at least some similarity with sequences identified as R43655 (yc86b04.s1 Homo sapiens cDNA clone 22829 3'), R50995 (yg63f06.s1 Homo sapiens cDNA clone 37377 3' similar to c ntains MER22 repetitive element), and W92748 (zd92h03.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 356981 3'). Based upon sequence similarity, 5 CJ145\_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of CJ145\_1 indicates that it may contain a CA simple repeat element.

#### Clone "CJ160\_11"

A polynucleotide of the present invention has been identified as clone "CJ160\_11". 10 CJ160\_11 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CJ160\_11 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CJ160\_11 protein").

15 The nucleotide sequence of CJ160\_11 as presently determined is reported in SEQ ID NO:162, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CJ160\_11 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:163. Amino acids 17 to 29 of SEQ ID NO:163 are a predicted leader/signal sequence, with the predicted mature amino acid sequence 20 beginning at amino acid 30. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CJ160\_11 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CJ160\_11 should be approximately 1700 bp.

25 The nucleotide sequence disclosed herein for CJ160\_11 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CJ160\_11 demonstrated at least some similarity with sequences identified as AA024511 (ze76e04.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 364926 3') and AC000074 (00884; HTGS phase 3, complete sequence). Based upon sequence similarity, 30 CJ160\_11 proteins and each similar protein or peptide may share at least some activity.

CJ160\_11 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 96 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

35 Clone "CO20\_1"

A polynucleotide of the present invention has been identified as clone "CO20\_1". CO20\_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CO20\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CO20\_1 protein").

The nucleotide sequence of the 5' portion of CO20\_1 as presently determined is reported in SEQ ID NO:164. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:165. The predicted amino acid sequence of the CO20\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:165. Amino acids 17 to 29 of SEQ ID NO:165 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 30. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CO20\_1 protein. Additional nucleotide sequence from the 3' portion of CO20\_1, including a poly(A) tail, is reported in SEQ ID NO:166.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CO20\_1 should be approximately 2400 bp.

The nucleotide sequence disclosed herein for CO20\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CO20\_1 demonstrated at least some similarity with sequences identified as AA045770 (zl68b10.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 509755 3' similar to SW:R13A\_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A), AA070899 (zm66c01.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone 530592 3' similar to contains Alu repetitive element), AA325205 (EST28155 Cerebellum II Homo sapiens cDNA 5' end), N22253 (yw36a08.s1 Homo sapiens cDNA clone 254294 3' similar to SP S29539 S29539 BASIC PROTEIN, 23K), R01933 (ye85g07.s1 Homo sapiens cDNA clone 124572 3' similar to SP:S29539 S29539 BASIC PROTEIN, 23K), R12008 (yf51f04.r1 Homo sapiens cDNA clone 25456 5'), R39848 (yf51f04.s1 Homo sapiens cDNA clone 25456 3' similar to contains Alu repetitive element; contains PTR5 repetitive element), R56565 (yg91c12.r1 Homo sapiens cDNA clone 40891 5'), T19487 (Human gene signature HUMGS00543), T30988 (EST25695 Homo sapiens cDNA 5' end similar to None), U37026 (Rattus norvegicus brain sodium channel beta 2 subunit (SCNB2) mRNA, complete cds), and X56932 (H.sapiens mRNA for 23 kD highly basic protein). The predicted amino acid sequence disclosed herein for CO20\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol.

The predicted CO20\_1 protein demonstrated at least some similarity to sequences identified as U37026 (sodium channel beta 2 subunit [Rattus norvegicus]), U58658 (unknown [Homo sapiens]), and X56932 (23 kD highly basic protein [Homo sapiens]). The sodium channel beta 2 subunit is a glycoprotein with an extracellular domain containing an immunoglobulin-like fold with  
5 similarity to the neural cell adhesion molecule contactin. Based upon sequence similarity, CO20\_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of CO20\_1 indicates that it may contain an Alu repetitive element.

#### Clone "CO223\_3"

10 A polynucleotide of the present invention has been identified as clone "CO223\_3". CO223\_3 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CO223\_3 is a full-length clone, including the entire coding sequence of  
15 a secreted protein (also referred to herein as "CO223\_3 protein").

The nucleotide sequence of CO223\_3 as presently determined is reported in SEQ ID NO:167, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CO223\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:168. Amino acids 35 to 47 of SEQ ID  
20 NO:168 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 48. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CO223\_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
25 CO223\_3 should be approximately 700 bp.

The nucleotide sequence disclosed herein for CO223\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CO223\_3 demonstrated at least some similarity with sequences identified as AA004498 (zh87b06.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 428243  
30 5' similar to. gb M62505 C5A ANAPHYLATOXIN CHEMOTACTIC RECEPTOR (HUMAN);contains L1.t1 L1 repetitive element) and U47924 (Human chromosome 12p13 gene cluster, surface antigen CD4 (CD4), A, B, G-protein beta-3 subunit (GNB3), isopeptidase T (ISOT) and triosephosphate isomerase (TPI) genes, complete cds). Based upon sequence similarity, CO223\_3 proteins and each similar protein or peptide may share at least some activity.

The 3' end of the CO223\_3 polynucleotide sequence contains a 54-bp sequence that is repeated three times in the clone; these repeats begin at positions 314, 368, and 422 of SEQ ID NO:167 and encode amino acids 47 to 64, 65 to 82, and 83 to 99 of SEQ ID NO:168, respectively.

5        Clone "CO310\_2"

A polynucleotide of the present invention has been identified as clone "CO310\_2". CO310\_2 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence  
10 of the encoded protein. CO310\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CO310\_2 protein").

The nucleotide sequence of CO310\_2 as presently determined is reported in SEQ ID NO:169, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CO310\_2 protein corresponding to the  
15 foregoing nucleotide sequence is reported in SEQ ID NO:170.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CO310\_2 should be approximately 1400 bp.

The nucleotide sequence disclosed herein for CO310\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search  
20 protocols. No hits were found in the database. The nucleotide sequence of CO310\_2 indicates that it may contain an L1 repetitive element.

Clone "CP258\_3"

A polynucleotide of the present invention has been identified as clone "CP258\_3".  
25 CP258\_3 was isolated from a human adult salivary gland cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CP258\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CP258\_3 protein").

The nucleotide sequence of CP258\_3 as presently determined is reported in SEQ ID NO:171, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CP258\_3 protein corresponding to the  
30 foregoing nucleotide sequence is reported in SEQ ID NO:172. Amino acids 3 to 15 of SEQ ID NO:172 are a predicted leader/signal sequence, with the predicted mature amino acid sequence  
35 beginning at amino acid 16. Due to the hydrophobic nature of the predicted leader/signal



sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CP258\_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CP258\_3 should be approximately 560 bp.

5       The nucleotide sequence disclosed herein for CP258\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database.

CP258\_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 26 kDa was detected in conditioned medium and membrane fractions using  
10   SDS polyacrylamide gel electrophoresis.

Clone "CW1155\_3"

A polynucleotide of the present invention has been identified as clone "CW1155\_3". CW1155\_3 was isolated from a human fetal brain cDNA library using methods which are  
15   selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CW1155\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CW1155\_3 protein").

The nucleotide sequence of CW1155\_3 as presently determined is reported in SEQ ID  
20   NO:173, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CW1155\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:174. Amino acids 220 to 232 of SEQ ID NO:174 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 233. Due to the hydrophobic nature of the predicted leader/signal  
25   sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CW1155\_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CW1155\_3 should be approximately 1170 bp.

The nucleotide sequence disclosed herein for CW1155\_3 was searched against the  
30   GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CW1155\_3 demonstrated at least some similarity with sequences identified as AA169043 (ms36h08.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone 613695 5'), D86145 (Rat mRNA), and H29261 (ym32b03.s1 Homo sapiens cDNA clone 49733 3'). Based upon sequence similarity, CW1155\_3 proteins and each similar protein or peptide may share at  
35   least some activity.

Clone "CZ247\_2"

A polynucleotide of the present invention has been identified as clone "CZ247\_2". CZ247\_2 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding  
5 a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CZ247\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CZ247\_2 protein").

The nucleotide sequence of CZ247\_2 as presently determined is reported in SEQ ID NO:175, and includes a poly(A) tail. What applicants presently believe to be the proper reading  
10 frame and the predicted amino acid sequence of the CZ247\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:176. Amino acids 545 to 557 of SEQ ID NO:176 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 558. Due to the hydrophobic nature of the predicted leader/signal  
15 sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CZ247\_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CZ247\_2 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for CZ247\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search  
20 protocols. CZ247\_2 demonstrated at least some similarity with sequences identified as T09256 (Human ara Kb beta-galactosidase fusion protein coding sequence), W27222 (26h9 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA), and W72736 (zd71e02.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 346106 3'). The predicted amino acid sequence disclosed herein for CZ247\_2 was searched against the GenPept and GeneSeq amino acid  
25 sequence databases using the BLASTX search protocol. The predicted CZ247\_2 protein demonstrated at least some similarity to sequences identified as R88069 (Human ara Kb beta-galactosidase fusion protein). Based upon sequence similarity, CZ247\_2 proteins and each similar protein or peptide may share at least some activity.

30 Clone "AM666\_1"

A polynucleotide of the present invention has been identified as clone "AM666\_1". AM666\_1 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino

acid sequence of the encoded protein. AM666\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AM666\_1 protein").

The nucleotide sequence of AM666\_1 as presently determined is reported in SEQ ID NO:177, and includes a poly(A) tail. What applicants presently believe to be the proper reading  
5 frame and the predicted amino acid sequence of the AM666\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:178. Amino acids 15 to 27 of SEQ ID NO:178 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 28. Due to the hydrophobic nature of the predicted leader/signal  
10 sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the AM666\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AM666\_1 should be approximately 1300 bp.

The nucleotide sequence disclosed herein for AM666\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA  
15 search protocols. AM666\_1 demonstrated at least some similarity with sequences identified as AA493985 (nh07g08.s1 NCI\_CGAP\_Thy1 Homo sapiens cDNA clone). Based upon sequence similarity, AM666\_1 proteins and each similar protein or peptide may share at least some activity.

AM666\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 17 kDa was detected in membrane fractions using SDS polyacrylamide gel  
20 electrophoresis.

#### Clone "BN387\_3"

A polynucleotide of the present invention has been identified as clone "BN387\_3". BN387\_3 was isolated from a human adult placenta cDNA library using methods which are  
25 selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BN387\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BN387\_3 protein").

The nucleotide sequence of BN387\_3 as presently determined is reported in SEQ ID  
30 NO:179, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BN387\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:180. Amino acids 14 to 26 of SEQ ID NO:180 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 27. Due to the hydrophobic nature of the predicted leader/signal

sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the BN387\_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BN387\_3 should be approximately 2000 bp.

5       The nucleotide sequence disclosed herein for BN387\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BN387\_3 demonstrated at least some similarity with sequences identified as H16912 (ym39d01.r1 Homo sapiens cDNA clone 50771 5'). Based upon sequence similarity, BN387\_3 proteins and each similar protein or peptide may share at least some activity.

10       BN387\_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 30 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

#### Clone "BQ135\_2"

15       A polynucleotide of the present invention has been identified as clone "BQ135\_2". BQ135\_2 was isolated from a human adult colon (adenocarcinoma Caco2) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BQ135\_2 is a full-length clone,  
20       including the entire coding sequence of a secreted protein (also referred to herein as "BQ135\_2 protein").

      The nucleotide sequence of BQ135\_2 as presently determined is reported in SEQ ID NO:181, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BQ135\_2 protein corresponding to the  
25       foregoing nucleotide sequence is reported in SEQ ID NO:182.

      The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BQ135\_2 should be approximately 1200 bp.

      The nucleotide sequence disclosed herein for BQ135\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search  
30       protocols. BQ135\_2 demonstrated at least some similarity with sequences identified as AA023751 (mh81f01.r1 Soares mouse placenta 4NbMP13.5 14.5 Mus musculus cDNA clone 457369 5'), AA105433 (ml83g01.r1 Stratagene mouse kidney (#937315) Mus musculus cDNA clone 518640 5'), D64061 (Rat brain mRNA for annexin V-binding protein (ABP-7), partial cds), and N67257 (yz49b08.s1 Homo sapiens cDNA clone 286359 3'). The predicted amino acid  
35       sequence disclosed herein for BQ135\_2 was searched against the GenPept and GeneSeq amino

acid sequence databases using the BLASTX search protocol. The predicted BQ135\_2 protein demonstrated at least some similarity to sequences identified as D64061 (annexin V-binding protein (ABP-7) [Rattus norvegicus]). Annexins associate with membranes and act as ion channels, they can also act as an autocrine factor that enhances osteoclast formation and bone resorption. Annexins have been localized in nucleoli and mitochondria but also in the cytoplasm, plasma (i.e. blood) and in association with vesicles. They are probably involved in fusing vesicles to each other and to plasma membranes causing secretion of vesicular contents. Specifically they have a calcium-dependent ability to bind phospholipids. Thus they are membrane associated. It is possible that annexin-binding proteins are also membrane associated even though they are highly hydrophilic through the same mechanism (electrostatic interaction with phospholipids of membranes). Based upon sequence similarity, BQ135\_2 proteins and each similar protein or peptide may share at least some activity.

#### Clone "CR678\_1"

A polynucleotide of the present invention has been identified as clone "CR678\_1". CR678\_1 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CR678\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CR678\_1 protein").

The nucleotide sequence of CR678\_1 as presently determined is reported in SEQ ID NO:183, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CR678\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:184.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CR678\_1 should be approximately 870 bp.

The nucleotide sequence disclosed herein for CR678\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CR678\_1 demonstrated at least some similarity with sequences identified as X85232 (H.sapiens chromosome 3 sequences). Based upon sequence similarity, CR678\_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of CR678\_1 indicates that it may contain an Alu repetitive element.

#### Clone "CW420\_2"

A polynucleotide of the present invention has been identified as clone "CW420\_2". CW420\_2 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CW420\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CW420\_2 protein").

The nucleotide sequence of CW420\_2 as presently determined is reported in SEQ ID NO:185, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CW420\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:186.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CW420\_2 should be approximately 5100 bp.

The nucleotide sequence disclosed herein for CW420\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CW420\_2 demonstrated at least some similarity with sequences identified as T55440 (yb38e09.s1 Homo sapiens cDNA clone 73480 3'). Based upon sequence similarity, CW420\_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the CW420\_2 protein sequence centered around amino acids 500 and 1270 of SEQ ID NO:186, respectively.

#### Clone "CW795\_2"

A polynucleotide of the present invention has been identified as clone "CW795\_2". CW795\_2 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CW795\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CW795\_2 protein").

The nucleotide sequence of CW795\_2 as presently determined is reported in SEQ ID NO:187, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CW795\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:188.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CW795\_2 should be approximately 3000 bp.

The nucleotide sequence disclosed herein for CW795\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA

search protocols. CW795\_2 demonstrated at least some similarity with sequences identified as AA115676 (zl86a09.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 511480 3'), N22955 (yw44h07.s1 Homo sapiens cDNA clone 255133 3'), and W56804 (zd16g06.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 340858 3'). The predicted amino acid sequence  
5 disclosed herein for CW795\_2 was searched against the GenPept, GeneSeq, and SwissProt amino acid sequence databases using the BLASTX search protocol. The predicted CW795\_2 protein demonstrated at least some similarity to sequences identified as X81068 (probable mitochondrial protein) and the yeast proteins rca1 and afg3 (tat-binding homologues). Based upon sequence similarity, CW795\_2 proteins and each similar protein or peptide may share at least some activity.  
10 The TopPredII computer program predicts two potential transmembrane domains within the CW795\_2 protein sequence centered around amino acids 60 and 170 of SEQ ID NO:188, respectively.

CW795\_2 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 10 kDa was detected in membrane fractions using SDS polyacrylamide gel  
15 electrophoresis.

#### Clone "CW823\_3"

A polynucleotide of the present invention has been identified as clone "CW823\_3". CW823\_3 was isolated from a human fetal brain cDNA library using methods which are selective  
20 for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CW823\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CW823\_3 protein").

The nucleotide sequence of CW823\_3 as presently determined is reported in SEQ ID  
25 NO:189, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CW823\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:190.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CW823\_3 should be approximately 600 bp.

30 The nucleotide sequence disclosed herein for CW823\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database.

Clone "DF989\_3"

A polynucleotide of the present invention has been identified as clone "DF989\_3". DF989\_3 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding  
5 a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. DF989\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "DF989\_3 protein").

The nucleotide sequence of the 5' portion of DF989\_3 as presently determined is reported in SEQ ID NO:191. What applicants presently believe is the proper reading frame for the coding  
10 region is indicated in SEQ ID NO:192. The predicted amino acid sequence of the DF989\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:192. Amino acids 2 to 14 of SEQ ID NO:192 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 15. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the  
15 predicted leader/signal sequence not be separated from the remainder of the DF989\_3 protein. Additional nucleotide sequence from the 3' portion of DF989\_3, including a poly(A) tail, is reported in SEQ ID NO:193.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone DF989\_3 should be approximately 1800 bp.

20 The nucleotide sequence disclosed herein for DF989\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. DF989\_3 demonstrated at least some similarity with sequences identified as R24724 (yg43c05.r1 Homo sapiens cDNA clone 35337 5') and T33717 (EST58870 Homo sapiens cDNA 5' end similar to None). Based upon sequence similarity, DF989\_3 proteins and each similar  
25 protein or peptide may share at least some activity.

Clone "DL162\_1"

A polynucleotide of the present invention has been identified as clone "DL162\_1". DL162\_1 was isolated from a human adult brain cDNA library using methods which are selective  
30 for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. DL162\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "DL162\_1 protein").

The nucleotide sequence of DL162\_1 as presently determined is reported in SEQ ID  
35 NO:194, and includes a poly(A) tail. What applicants presently believe to be the proper reading



frame and the predicted amino acid sequence of the DL162\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:195. Amino acids 28 to 40 of SEQ ID NO:195 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 41. Due to the hydrophobic nature of the predicted leader/signal  
5 sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the DL162\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone DL162\_1 should be approximately 875 bp.

The nucleotide sequence disclosed herein for DL162\_1 was searched against the GenBank  
10 and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database.

#### Clone "DL162\_2"

A polynucleotide of the present invention has been identified as clone "DL162\_2".  
15 DL162\_2 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. DL162\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "DL162\_2 protein").

20 The nucleotide sequence of DL162\_2 as presently determined is reported in SEQ ID NO:196, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the DL162\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:197. Amino acids 1 to 13 of SEQ ID  
25 NO:197 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 14. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the DL162\_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone DL162\_2 should be approximately 4000 bp.

30 The predicted amino acid sequence disclosed herein for DL162\_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted DL162\_2 protein demonstrated at least some similarity to sequences identified as AB002309 (KIAA0311 protein [Homo sapiens]). The TopPredII computer program predicts a potential transmembrane domains within the DL162\_2 protein sequence near the carboxyl  
35 terminus of SEQ ID NO:197.

DL162\_2 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 160 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

5        Clone "EC172\_1"

A polynucleotide of the present invention has been identified as clone "EC172\_1". EC172\_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. EC172\_1 is a full-length clone, including the entire coding sequence of  
10        a secreted protein (also referred to herein as "EC172\_1 protein").

The nucleotide sequence of EC172\_1 as presently determined is reported in SEQ ID NO:198, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the EC172\_1 protein corresponding to the  
15        foregoing nucleotide sequence is reported in SEQ ID NO:199. Amino acids 659 to 671 of SEQ ID NO:199 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 672. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the EC172\_1 protein.

20        The EcoRI/NotI restriction fragment obtainable from the deposit containing clone EC172\_1 should be approximately 4000 bp.

The nucleotide sequence disclosed herein for EC172\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. EC172\_1 demonstrated at least some similarity with sequences identified as H31192  
25        (EST104991 Rattus sp. cDNA 3' end similar to C.elegans hypothetical protein ZK1098.10) and U29585 (Streptococcus pyogenes emm18.1). The predicted amino acid sequence disclosed herein for EC172\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted EC172\_1 protein demonstrated at least some similarity to sequences identified as Z22176 (ZK1098.10 [Caenorhabditis elegans]). Based upon  
30        sequence similarity, EC172\_1 proteins and each similar protein or peptide may share at least some activity.

Deposit of Clones

Clones AX65\_22, BD335\_14, BG241\_1, BL187\_4, BL249\_18, BO71\_1, BO365\_2,  
35        BV51\_1, BV140\_3, BV141\_2, CC194\_4, and DA136\_11 were deposited on October 3, 1996 with

the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98196, from which each clone comprising a particular polynucleotide is obtainable.

5 Clones AR415\_4, AS63\_29, BG160\_1, BO432\_4, BO538\_2, BR595\_4, CI490\_2, CI522\_1, CN238\_1, CO390\_1, and AY304\_1 (an additional isolate of clone AY304\_14) were deposited on October 25, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98232, from which each clone comprising  
10 a particular polynucleotide is obtainable. Clone AY304\_14 was deposited on October 23, 1997 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and was given the accession number 98561.

Clones AJ20\_2, AR440\_1, AS164\_1, AX8\_1, BD176\_3, BD339\_1, BD427\_1, BL229\_22,  
15 BV123\_16, and CH377\_1 were deposited on November 15, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98261, from which each clone comprising a particular polynucleotide is obtainable.

Clones BD441\_1, BD441\_2, BG102\_3, BK158\_1, BP163\_1, BZ16\_3, CC182\_1,  
20 CG109\_1 and CJ397\_1 were deposited on November 20, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98264, from which each clone comprising a particular polynucleotide is obtainable.

Clones AM795\_4, AT340\_1, BG132\_1, BG219\_2, BG366\_2, BV172\_2, CC247\_10,  
25 CI480\_9, CO722\_1, and CT748\_2 were deposited on December 5, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98271, from which each clone comprising a particular polynucleotide is obtainable.

Clones AJ1\_1, AQ73\_3, BG142\_1, BV66\_1, BV291\_3, CK201\_1, CQ331\_2, CT550\_1,  
30 CT585\_1 and CT797\_3 were deposited on December 13, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98278, from which each clone comprising a particular polynucleotide is obtainable.

Clones CB107\_1, CG300\_3, CJ145\_1, CJ160\_11, CO20\_1, CO223\_1, CO310\_2,  
35 CP258\_3, CW1155\_3 and CZ247\_2 were deposited on December 17, 1996 with the ATCC

(American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98279, from which each clone comprising a particular polynucleotide is obtainable. Clone CO223\_3 was deposited on January 9, 1997 with the ATCC (American Type Culture Collection, 5 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and was given the accession number 98291.

Clones AM666\_1, BN387\_3, BQ135\_2, CR678\_1, CW420\_2, CW795\_2, CW823\_3, DF989\_3, DL162\_2, DL162\_1, and EC172\_1 were deposited on January 10, 1997 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 10 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98292, from which each clone comprising a particular polynucleotide is obtainable.

All restrictions on the availability to the public of the deposited material will be irrevocably removed upon the granting of the patent, except for the requirements specified in 37 C.F.R. § 1.808(b), and the term of the deposit will comply with 37 C.F.R. § 1.806.

15 Each clone has been transfected into separate bacterial cells (*E. coli*) in this composite deposit. Each clone can be removed from the vector in which it was deposited by performing an EcoRI/NotI digestion (5' site, EcoRI; 3' site, NotI) to produce the appropriate fragment for such clone. Each clone was deposited in either the pED6 or pNOTs vector depicted in Figures 1A and 1B, respectively. The pED6dpc2 vector ("pED6") was derived from pED6dpc1 by insertion of 20 a new polylinker to facilitate cDNA cloning (Kaufman *et al.*, 1991, *Nucleic Acids Res.* 19: 4485-4490); the pNOTs vector was derived from pMT2 (Kaufman *et al.*, 1989, *Mol. Cell. Biol.* 9: 946-958) by deletion of the DHFR sequences, insertion of a new polylinker, and insertion of the M13 origin of replication in the ClaI site. In some instances, the deposited clone can become "flipped" (i.e., in the reverse orientation) in the deposited isolate. In such instances, the cDNA insert can 25 still be isolated by digestion with EcoRI and NotI. However, NotI will then produce the 5' site and EcoRI will produce the 3' site for placement of the cDNA in proper orientation for expression in a suitable vector. The cDNA may also be expressed from the vectors in which they were deposited.

Bacterial cells containing a particular clone can be obtained from the composite deposit 30 as follows:

An oligonucleotide probe or probes should be designed to the sequence that is known for that particular clone. This sequence can be derived from the sequences provided herein, or from a combination of those sequences. The sequence of an oligonucleotide probe that was used to isolate or to sequence each full-length clone is identified below, and should be most reliable in 35 isolating the clone of interest.

	<u>Clone</u>	<u>Probe Sequence</u>
	AX65_22	SEQ ID NO:200
	BD335_14	SEQ ID NO:201
	BG241_1	SEQ ID NO:202
5	BL187_4	SEQ ID NO:203
	BL249_18	SEQ ID NO:204
	BO71_1	SEQ ID NO:205
	BO365_2	SEQ ID NO:206
	BV51_1	SEQ ID NO:207
10	BV140_3	SEQ ID NO:208
	BV141_2	SEQ ID NO:209
	CC194_4	SEQ ID NO:210
	DA136_11	SEQ ID NO:211
	AR415_4	SEQ ID NO:212
15	AS63_29	SEQ ID NO:213
	AY304_14	SEQ ID NO:214
	BG160_1	SEQ ID NO:215
	BO432_4	SEQ ID NO:216
	BO538_2	SEQ ID NO:217
20	BR595_4	SEQ ID NO:218
	CI490_2	SEQ ID NO:219
	CI522_1	SEQ ID NO:220
	CN238_1	SEQ ID NO:221
	CO390_1	SEQ ID NO:222
25	AJ20_2	SEQ ID NO:223
	AR440_1	SEQ ID NO:224
	AS164_1	SEQ ID NO:225
	AX8_1	SEQ ID NO:226
	BD176_3	SEQ ID NO:227
30	BD339_1	SEQ ID NO:228
	BD427_1	SEQ ID NO:229
	BL229_22	SEQ ID NO:230
	BV123_16	SEQ ID NO:231
	CH377_1	SEQ ID NO:232
35	BD441_1	SEQ ID NO:233

	BD441_2	SEQ ID NO:234
	BG102_3	SEQ ID NO:235
	BK158_1	SEQ ID NO:236
	BP163_1	SEQ ID NO:237
5	BZ16_3	SEQ ID NO:238
	CC182_1	SEQ ID NO:239
	CG109_1	SEQ ID NO:240
	CJ397_1	SEQ ID NO:241
	AM795_4	SEQ ID NO:242
10	AT340_1	SEQ ID NO:243
	BG132_1	SEQ ID NO:244
	BG219_2	SEQ ID NO:245
	BG366_2	SEQ ID NO:246
	BV172_2	SEQ ID NO:247
15	CC247_10	SEQ ID NO:248
	CI480_9	SEQ ID NO:249
	CO722_1	SEQ ID NO:250
	CT748_2	SEQ ID NO:251
	AJ1_1	SEQ ID NO:252
20	AQ73_3	SEQ ID NO:253
	BG142_1	SEQ ID NO:254
	BV66_1	SEQ ID NO:255
	BV291_3	SEQ ID NO:256
	CK201_1	SEQ ID NO:257
25	CQ331_2	SEQ ID NO:258
	CT550_1	SEQ ID NO:259
	CT585_1	SEQ ID NO:260, SEQ ID NO:262
	CT797_3	SEQ ID NO:261
	CB107_1	SEQ ID NO:263
30	CG300_3	SEQ ID NO:264
	CJ145_1	SEQ ID NO:265
	CJ160_11	SEQ ID NO:266
	CO20_1	SEQ ID NO:267
	CO223_3	SEQ ID NO:268
35	CO310_2	SEQ ID NO:269

	CP258_3	SEQ ID NO:270
	CW1155_3	SEQ ID NO:271
	CZ247_2	SEQ ID NO:272
	AM666_1	SEQ ID NO:273
5	BN387_3	SEQ ID NO:274
	BQ135_2	SEQ ID NO:275
	CR678_1	SEQ ID NO:276
	CW420_2	SEQ ID NO:277
	CW795_2	SEQ ID NO:278
10	CW823_3	SEQ ID NO:279
	DF989_3	SEQ ID NO:280
	DL162_1, DL162_2	SEQ ID NO:281
	EC172_1	SEQ ID NO:282

15 In the sequences listed above which include an N at position 2, that position is occupied in preferred probes/primers by a biotinylated phosphoramidite residue rather than a nucleotide (such as, for example, that produced by use of biotin phosphoramidite (1-dimethoxytrityloxy-2-(N-biotinyl-4-aminobutyl)-propyl-3-O-(2-cyanoethyl)-(N,N-diisopropyl)-phosphoramidite) (Glen Research, cat. no. 10-1953)).

20 The design of the oligonucleotide probe should preferably follow these parameters:

- (a) It should be designed to an area of the sequence which has the fewest ambiguous bases ("N's"), if any;
- (b) It should be designed to have a  $T_m$  of approx. 80 ° C (assuming 2° for each A or T and 4 degrees for each G or C).

25 The oligonucleotide should preferably be labeled with  $\gamma$ -<sup>32</sup>P ATP (specific activity 6000 Ci/mmmole) and T4 polynucleotide kinase using commonly employed techniques for labeling oligonucleotides. Other labeling techniques can also be used. Unincorporated label should preferably be removed by gel filtration chromatography or other established methods. The amount of radioactivity incorporated into the probe should be quantitated by measurement in a

30 scintillation counter. Preferably, specific activity of the resulting probe should be approximately 4e+6 dpm/pmmole.

The bacterial culture containing the pool of full-length clones should preferably be thawed and 100  $\mu$ l of the stock used to inoculate a sterile culture flask containing 25 ml of sterile L-broth containing ampicillin at 100  $\mu$ g/ml. The culture should preferably be grown to saturation at 37°C,

35 and the saturated culture should preferably be diluted in fresh L-broth. Aliquots of these dilutions

should preferably be plated to determine the dilution and volume which will yield approximately 5000 distinct and well-separated colonies on solid bacteriological media containing L-broth containing ampicillin at 100 µg/ml and agar at 1.5% in a 150 mm petri dish when grown overnight at 37°C. Other known methods of obtaining distinct, well-separated colonies can also be employed.

Standard colony hybridization procedures should then be used to transfer the colonies to nitrocellulose filters and lyse, denature and bake them.

The filter is then preferably incubated at 65°C for 1 hour with gentle agitation in 6X SSC (20X stock is 175.3 g NaCl/liter, 88.2 g Na citrate/liter, adjusted to pH 7.0 with NaOH) containing 0.5% SDS, 100 µg/ml of yeast RNA, and 10 mM EDTA (approximately 10 mL per 150 mm filter). Preferably, the probe is then added to the hybridization mix at a concentration greater than or equal to 1e+6 dpm/mL. The filter is then preferably incubated at 65°C with gentle agitation overnight. The filter is then preferably washed in 500 mL of 2X SSC/0.5% SDS at room temperature without agitation, preferably followed by 500 mL of 2X SSC/0.1% SDS at room temperature with gentle shaking for 15 minutes. A third wash with 0.1X SSC/0.5% SDS at 65°C for 30 minutes to 1 hour is optional. The filter is then preferably dried and subjected to autoradiography for sufficient time to visualize the positives on the X-ray film. Other known hybridization methods can also be employed.

The positive colonies are picked, grown in culture, and plasmid DNA isolated using standard procedures. The clones can then be verified by restriction analysis, hybridization analysis, or DNA sequencing.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, *et al.*, Bio/Technology 10, 773-778 (1992) and in R.S. McDowell, *et al.*, J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decavalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form(s) of such protein



may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with the ATCC) in a suitable mammalian cell or other host cell. The sequence(s) of the mature form(s) of the protein may also be determinable from the amino acid sequence of the full-length form.

5           The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are derived and may include contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3'  
10   untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. An "isolated gene"  
15   is a gene that has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

          The chromosomal location corresponding to the polynucleotide sequences disclosed herein may also be determined, for example by hybridizing appropriately labeled polynucleotides of the present invention to chromosomes *in situ*. It may also be possible to determine the  
20   corresponding chromosomal location for a disclosed polynucleotide by identifying significantly similar nucleotide sequences in public databases, such as expressed sequence tags (ESTs), that have already been mapped to particular chromosomal locations. For at least some of the polynucleotide sequences disclosed herein, public database sequences having at least some similarity to the polynucleotide of the present invention have been listed by database accession  
25   number. Searches using the GenBank accession numbers of these public database sequences can then be performed at an Internet site provided by the National Center for Biotechnology Information having the address <http://www.ncbi.nlm.nih.gov/UniGene/>, in order to identify "UniGene clusters" of overlapping sequences. Many of the "UniGene clusters" so identified will already have been mapped to particular chromosomal sites.

30           Organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and Morris, 1994, *Trends Pharmacol. Sci.* 15(7): 250-254; Lavarosky *et al.*, 1997, *Biochem. Mol. Med.* 62(1): 11-22; and  
35   Hampel, 1998, *Prog. Nucleic Acid Res. Mol. Biol.* 58: 1-39; all of which are incorporated by

reference herein). The desired change in gene expression can also be achieved through the use of double-stranded ribonucleotide molecules having some complementarity to the mRNA transcribed from the gene, and which interfere with the transcription, stability, or expression of the mRNA ("RNA interference" or "RNAi"; Fire *et al.*, 1998, *Nature* 391 (6669): 806-811; 5 Montgomery *et al.*, 1998, *Proc. Natl. Acad. Sci. USA* 95 (26): 15502-15507; and Sharp, 1999, *Genes Dev.* 13 (2): 139-141; all of which are incorporated by reference herein). Transgenic animals that have multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided. Transgenic 10 animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous sequences into the 15 corresponding gene(s) or through deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished through insertion, preferably followed by imprecise excision, of transposable elements (Plasterk, 1992, *Bioessays* 14(9): 629-633; Zwaal *et al.*, 1993, *Proc. Natl. Acad. Sci. USA* 90(16): 7431-7435; Clark *et al.*, 1994, *Proc. Natl. Acad. Sci. USA* 91(2): 719-722; all of which are incorporated by reference herein), or through 20 homologous recombination, preferably detected by positive/negative genetic selection strategies (Mansour *et al.*, 1988, *Nature* 336: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614,396; 5,616,491; and 5,679,523; all of which are incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models 25 for the study of disorders involving the corresponding gene(s), and for the development of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s).

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms, part or all of the 30 intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information. For example, the TopPredII computer program can be used to predict the location of transmembrane domains in an amino acid sequence, domains

which are described by the location of the center of the transmembrane domain, with at least ten transmembrane amino acids on each side of the reported central residue(s).

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

In particular, sequence identity may be determined using WU-BLAST (Washington University BLAST) version 2.0 software, which builds upon WU-BLAST version 1.4, which in turn is based on the public domain NCBI-BLAST version 1.4 (Altschul and Gish, 1996, Local alignment statistics, Doolittle *ed.*, *Methods in Enzymology* 266: 460-480; Altschul *et al.*, 1990, Basic local alignment search tool, *Journal of Molecular Biology* 215: 403-410; Gish and States, 1993, Identification of protein coding regions by database similarity search, *Nature Genetics* 3: 266-272; Karlin and Altschul, 1993, Applications and statistics for multiple high-scoring segments in molecular sequences, *Proc. Natl. Acad. Sci. USA* 90: 5873-5877; all of which are incorporated by reference herein). WU-BLAST version 2.0 executable programs for several UNIX platforms can be downloaded from <ftp://blast.wustl.edu/blast/executables>. The complete suite of search programs (BLASTP, BLASTN, BLASTX, TBLASTN, and TBLASTX) is provided at that site, in addition to several support programs. WU-BLAST 2.0 is copyrighted and may not be sold or redistributed in any form or manner without the express written consent of the author; but the posted executables may otherwise be freely used for commercial, nonprofit, or academic purposes. In all search programs in the suite -- BLASTP, BLASTN, BLASTX, TBLASTN and TBLASTX -- the gapped alignment routines are integral to the database search itself, and thus yield much better sensitivity and selectivity while producing the more easily interpreted output. Gapping can optionally be turned off in all of these programs, if desired. The default penalty (Q) for a gap of length one is Q=9 for proteins

and BLASTP, and Q=10 for BLASTN, but may be changed to any integer value including zero, one through eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. The default per-residue penalty for extending a gap (R) is R=2 for proteins and BLASTP, and R=10 for BLASTN, but may be changed to any integer value including zero, one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. Any combination of values for Q and R can be used in order to align sequences so as to maximize overlap and identity while minimizing sequence gaps. The default amino acid comparison matrix is BLOSUM62, but other amino acid comparison matrices such as PAM can be utilized.

Species homologues of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide. Preferably, polynucleotide species homologues have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, and protein species homologues have at least 30% sequence identity (more preferably, at least 45% identity; most preferably at least 60% identity) with the given protein, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides or the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Species homologues may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species. Preferably, species homologues are those isolated from mammalian species. Most preferably, species homologues are those isolated from certain mammalian species such as, for example, *Pan troglodytes*, *Gorilla gorilla*, *Pongo pygmaeus*, *Hylobates concolor*, *Macaca mulatta*, *Papio papio*, *Papio hamadryas*, *Cercopithecus aethiops*, *Cebus capucinus*, *Aotus trivirgatus*, *Sanguinus oedipus*, *Microcebus murinus*, *Mus musculus*, *Rattus norvegicus*, *Cricetulus griseus*, *Felis catus*, *Mustela vison*, *Canis familiaris*, *Oryctolagus cuniculus*, *Bos taurus*, *Ovis aries*, *Sus scrofa*, and *Equus caballus*, for which genetic maps have been created allowing the identification of syntenic relationships between the genomic organization of genes in one species and the genomic organization of the related genes in another species (O'Brien and Seuánez, 1988, *Ann. Rev. Genet.* 22: 323-351; O'Brien *et al.*, 1993, *Nature Genetics* 3:103-112; Johansson *et al.*, 1995, *Genomics* 25: 682-690; Lyons *et al.*, 1997, *Nature Genetics* 15: 47-56; O'Brien *et al.*, 1997, *Trends in Genetics* 13(10): 393-399; Carver and Stubbs, 1997, *Genome Research* 7:1123-1137; all of which are incorporated by reference herein).

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotides which also encode proteins which are identical or have significantly similar sequences to those encoded by the disclosed polynucleotides. Preferably, allelic variants have at least 60% sequence identity  
5 (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. Allelic variants may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic  
10 acid source from individuals of the appropriate species.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides that hybridize under reduced stringency conditions, more preferably stringent conditions, and most preferably highly stringent  
15 conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the table below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) <sup>‡</sup>	Hybridization Temperature and Buffer <sup>†</sup>	Wash Temperature and Buffer <sup>†</sup>
5	A	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	B	<50	T <sub>B</sub> *; 1xSSC	T <sub>B</sub> *; 1xSSC
	C	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	D	<50	T <sub>D</sub> *; 1xSSC	T <sub>D</sub> *; 1xSSC
	E	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
	F	<50	T <sub>F</sub> *; 1xSSC	T <sub>F</sub> *; 1xSSC
10	G	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	H	<50	T <sub>H</sub> *; 4xSSC	T <sub>H</sub> *; 4xSSC
	I	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	J	<50	T <sub>J</sub> *; 4xSSC	T <sub>J</sub> *; 4xSSC
	K	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	<50	T <sub>L</sub> *; 2xSSC	T <sub>L</sub> *; 2xSSC
15	M	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	<50	T <sub>N</sub> *; 6xSSC	T <sub>N</sub> *; 6xSSC
	O	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
	P	<50	T <sub>P</sub> *; 6xSSC	T <sub>P</sub> *; 6xSSC
	Q	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	R	<50	T <sub>R</sub> *; 4xSSC	T <sub>R</sub> *; 4xSSC

<sup>‡</sup>: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

<sup>†</sup>: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH<sub>2</sub>PO<sub>4</sub>, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

\*T<sub>B</sub> - T<sub>R</sub>: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T<sub>m</sub>) of the hybrid, where T<sub>m</sub> is determined according to the following equations. For hybrids less than 18 base pairs in length, T<sub>m</sub>(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T<sub>m</sub>(°C) = 81.5 + 16.6(log<sub>10</sub>[Na<sup>+</sup>]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na<sup>+</sup>] is the concentration of sodium ions in the hybridization buffer ([Na<sup>+</sup>] for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory*

*Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

The isolated polynucleotide encoding the protein of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman *et al.*, *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, California, U.S.A. (the  
5 MaxBac® kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under  
10 culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-  
15 toyopearl® or Cibacrom blue 3GA Sepharose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of  
20 maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLabs (Beverly, MA), Pharmacia (Piscataway, NJ) and Invitrogen Corporation (Carlsbad, CA), respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available  
25 from the Eastman Kodak Company (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially  
30 homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic animals, *e.g.*, as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized  
35 by somatic or germ cells containing a nucleotide sequence encoding the protein.



The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

#### **USES AND BIOLOGICAL ACTIVITY**

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

##### **Research Uses and Utilities**

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding

protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, those described in Gyuris *et al.*, 1993, *Cell* 75: 791-803 and in Rossi *et al.*, 1997, *Proc. Natl. Acad. Sci. USA* 94: 8405-8410, all of which are incorporated by reference herein) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

### Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate.

5 In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

10

### Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date,

15 including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2,

20 CTLL2, TF-1, Mo7e and CMK. The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In

25 Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., J. Immunol. 149:3778-3783, 1992; Bowman et al., J. Immunol. 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or

30 thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon  $\gamma$ , Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991;

5 deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark,

10 S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins

15 that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic

20 studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

#### Immune Stimulating or Suppressing Activity

25 A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells

30 and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as

candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, 5 rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression 10 is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to regulate immune responses in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The 15 functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists 20 after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), *e.g.*, preventing high level 25 lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule 30 which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the 35 corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter

prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosis in MRL/*lpr/lpr* mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral

diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed  
5 APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and  
10 reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a  
15 nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like  
20 activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells  
25 to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I  $\alpha$  chain protein and  $\beta_2$  microglobulin protein or an MHC class II  $\alpha$  chain protein and an MHC  
30 class II  $\beta$  chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant  
35 chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B

lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the  
5 following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic  
10 studies in Humans); Herrmann et al., *Proc. Natl. Acad. Sci. USA* 78:2488-2492, 1981; Herrmann et al., *J. Immunol.* 128:1968-1974, 1982; Handa et al., *J. Immunol.* 135:1564-1572, 1985; Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Herrmann et al., *Proc. Natl. Acad. Sci. USA* 78:2488-2492, 1981; Herrmann et al., *J. Immunol.* 128:1968-1974, 1982; Handa et al., *J. Immunol.* 135:1564-1572, 1985; Takai et al., *J. Immunol.*  
15 137:3494-3500, 1986; Bowman et al., *J. Virology* 61:1992-1998; Takai et al., *J. Immunol.* 140:508-512, 1988; Bertagnoli et al., *Cellular Immunology* 133:327-341, 1991; Brown et al., *J. Immunol.* 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect  
20 Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, *J. Immunol.* 144:3028-3033, 1990; and Assays for B cell function: *In vitro* antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins  
25 that generate predominantly Th1 and CTL responses) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512,  
30 1988; Bertagnoli et al., *J. Immunol.* 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., *J. Immunol.* 134:536-544, 1995; Inaba et al., *Journal of Experimental Medicine* 173:549-559, 1991; Macatonia et al., *Journal of Immunology* 154:5071-5079, 1995; Porgador et al., *Journal of Experimental Medicine* 182:255-260, 1995; Nair et al., *Journal of Virology*  
35



67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

#### Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow

transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

5            Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. *Cellular Biology* 15:141-151, 1995; Keller et al., *Molecular and*  
10 *Cellular Biology* 13:473-486, 1993; McClanahan et al., *Blood* 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al.,  
15 *Proc. Natl. Acad. Sci. USA* 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 1-21,  
20 Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

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#### Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

30            A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an

osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming  
5 cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

10 Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a  
15 tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also  
20 useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention  
25 may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral  
30 nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral  
35 sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with

the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

### Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin  $\alpha$  family, may be useful as a contraceptive based on the ability of

inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- $\beta$  group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., *Endocrinology* 91:562-572, 1972; Ling et al., *Nature* 321:779-782, 1986; Vale et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986.

#### Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation,

- those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

#### Hemostatic and Thrombolytic Activity

- A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

- Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

#### Receptor/Ligand Activity

- A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

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#### Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

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#### Cadherin/Tumor Invasion Suppressor Activity

Cadherins are calcium-dependent adhesion molecules that appear to play major roles during development, particularly in defining specific cell types. Loss or alteration of normal cadherin expression can lead to changes in cell adhesion properties linked to tumor growth and metastasis. Cadherin malfunction is also implicated in other human diseases, such as pemphigus vulgaris and pemphigus foliaceus (auto-immune blistering skin diseases), Crohn's disease, and some developmental abnormalities.

The cadherin superfamily includes well over forty members, each with a distinct pattern of expression. All members of the superfamily have in common conserved extracellular repeats (cadherin domains), but structural differences are found in other parts of the molecule. The

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cadherin domains bind calcium to form their tertiary structure and thus calcium is required to mediate their adhesion. Only a few amino acids in the first cadherin domain provide the basis for homophilic adhesion; modification of this recognition site can change the specificity of a cadherin so that instead of recognizing only itself, the mutant molecule can now also bind to a different cadherin. In addition, some cadherins engage in heterophilic adhesion with other cadherins.

E-cadherin, one member of the cadherin superfamily, is expressed in epithelial cell types. Pathologically, if E-cadherin expression is lost in a tumor, the malignant cells become invasive and the cancer metastasizes. Transfection of cancer cell lines with polynucleotides expressing E-cadherin has reversed cancer-associated changes by returning altered cell shapes to normal, restoring cells' adhesiveness to each other and to their substrate, decreasing the cell growth rate, and drastically reducing anchorage-independent cell growth. Thus, reintroducing E-cadherin expression reverts carcinomas to a less advanced stage. It is likely that other cadherins have the same invasion suppressor role in carcinomas derived from other tissue types. Therefore, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to treat cancer. Introducing such proteins or polynucleotides into cancer cells can reduce or eliminate the cancerous changes observed in these cells by providing normal cadherin expression.

Cancer cells have also been shown to express cadherins of a different tissue type than their origin, thus allowing these cells to invade and metastasize in a different tissue in the body. Proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be substituted in these cells for the inappropriately expressed cadherins, restoring normal cell adhesive properties and reducing or eliminating the tendency of the cells to metastasize.

Additionally, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to generate antibodies recognizing and binding to cadherins. Such antibodies can be used to block the adhesion of inappropriately expressed tumor-cell cadherins, preventing the cells from forming a tumor elsewhere. Such an anti-cadherin antibody can also be used as a marker for the grade, pathological type, and prognosis of a cancer, i.e. the more progressed the cancer, the less cadherin expression there will be, and this decrease in cadherin expression can be detected by the use of a cadherin-binding antibody.

Fragments of proteins of the present invention with cadherin activity, preferably a polypeptide comprising a decapeptide of the cadherin recognition site, and polynucleotides of the present invention encoding such protein fragments, can also be used to block cadherin function by binding to cadherins and preventing them from binding in ways that produce undesirable effects. Additionally, fragments of proteins of the present invention with cadherin activity,



preferably truncated soluble cadherin fragments which have been found to be stable in the circulation of cancer patients, and polynucleotides encoding such protein fragments, can be used to disturb proper cell-cell adhesion.

Assays for cadherin adhesive and invasive suppressor activity include, without limitation, those described in: Hortsch et al. J Biol Chem 270 (32): 18809-18817, 1995; Miyaki et al. Oncogene 11: 2547-2552, 1995; Ozawa et al. Cell 63: 1033-1038, 1990.

#### Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via antibody-dependent cell-mediated cytotoxicity (ADCC)). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

#### Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an

immune response against such protein or another material or entity which is cross-reactive with such protein.

#### **ADMINISTRATION AND DOSING**

5           A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable"

10 means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2,

15 G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in

20 formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

          A protein of the present invention may be active in multimers (e.g., heterodimers or

25 homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

          The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will

30 respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with

35 co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind

surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous,

intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01  $\mu$ g

to about 100 mg (preferably about 0.1mg to about 10 mg, more preferably about 0.1 µg to about 1 mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. As used herein, the term "antibody" includes without limitation a polyclonal antibody, a monoclonal antibody, a chimeric antibody, a single-chain antibody, a CDR-grafted antibody, a humanized antibody, or fragments thereof which bind to the indicated protein. Such term also includes any other species derived from an antibody or antibody sequence which is capable of binding the indicated protein.

Antibodies to a particular protein can be produced by methods well known to those skilled in the art. For example, monoclonal antibodies can be produced by generation of antibody-producing hybridomas in accordance with known methods (see for example, Goding, 1983, Monoclonal antibodies: principles and practice, Academic Press Inc., New York; and Yokoyama, 1992, "Production of Monoclonal Antibodies" in Current Protocols in Immunology, Unit 2.5, Greene Publishing Assoc. and John Wiley & Sons). Polyclonal sera and antibodies can be produced by inoculation of a mammalian subject with the relevant protein or fragments thereof in accordance with known methods. Fragments of antibodies, receptors, or other reactive peptides can be produced from the corresponding antibodies by cleavage of and collection of the desired fragments in accordance with known methods (see for example, Goding, supra; and Andrew et al., 1992, "Fragmentation of Immunoglobulins" in Current Protocols in Immunology, Unit 2.8, Greene Publishing Assoc. and John Wiley & Sons). Chimeric antibodies and single chain antibodies can also be produced in accordance with known recombinant methods (see for example, 5,169,939, 5,194,594, and 5,576,184). Humanized antibodies can also be made from corresponding murine antibodies in accordance with well known methods (see for

example, U.S. Patent Nos. 5,530,101, 5,585,089, and 5,693,762). Additionally, human antibodies may be produced in non-human animals such as mice that have been genetically altered to express human antibody molecules (see for example Fishwild *et al.*, 1996, *Nature Biotechnology* 14: 845-851; Mendez *et al.*, 1997, *Nature Genetics* 15: 146-156 (erratum *Nature Genetics* 16: 410); and U.S. Patents 5,877,397 and 5,625,126). Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer.Chem.Soc. 85, 2149-2154 (1963); J.L. Krstenansky, *et al.*, FEBS Lett. 211, 10 (1987).

Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite,

polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue

(e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final  
5 composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a  
10 mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can  
15 then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.



What is claimed is:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:41;
- (b) the nucleotide sequence of SEQ ID NO:41 from nucleotide 102 to nucleotide 2027;
- (c) the nucleotide sequence of SEQ ID NO:41 from nucleotide 1902 to nucleotide 2027;
- (d) the nucleotide sequence of SEQ ID NO:41 from nucleotide 1 to nucleotide 431;
- (e) the nucleotide sequence of the full-length protein coding sequence of clone BG160\_1 deposited with the ATCC under accession number 98232;
- (f) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone BG160\_1 deposited with the ATCC under accession number 98232;
- (g) the nucleotide sequence of a mature protein coding sequence of clone BG160\_1 deposited with the ATCC under accession number 98232;
- (h) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone BG160\_1 deposited with the ATCC under accession number 98232;
- (i) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:42;
- (j) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42;
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h); and
- (l) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h), and that has a length that is at least 25% of the length of SEQ ID NO:41.

2. The polynucleotide of claim 1 wherein said polynucleotide is operably linked to at least one expression control sequence.

3. A host cell transformed with the polynucleotide of claim 2.

4. The host cell of claim 3, wherein said cell is a mammalian cell.
5. A process for producing a protein encoded by the polynucleotide of claim 2, which process comprises:
  - (a) growing a culture of a host cell in a suitable culture medium, wherein the host cell has been transformed with the polynucleotide of claim 2; and
  - (b) purifying said protein from the culture.
6. A protein produced according to the process of claim 5.
7. An isolated polynucleotide encoding the protein of claim 6.
8. The polynucleotide of claim 7, wherein the polynucleotide comprises the cDNA insert of clone BG160\_1 deposited with the ATCC under accession number 98232.
9. A protein comprising an amino acid sequence selected from the group consisting of:
  - (a) the amino acid sequence of SEQ ID NO:42;
  - (b) the amino acid sequence of SEQ ID NO:42 from amino acid 1 to amino acid 110;
  - (c) a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42; and
  - (d) the amino acid sequence encoded by the cDNA insert of clone BG160\_1 deposited with the ATCC under accession number 98232;the protein being substantially free from other mammalian proteins.
10. The protein of claim 9, wherein said protein comprises the amino acid sequence of SEQ ID NO:42.
11. A composition comprising the protein of claim 9 and a pharmaceutically acceptable carrier.
12. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
  - (a) the nucleotide sequence of SEQ ID NO:129;

- (b) the nucleotide sequence of SEQ ID NO:129 from nucleotide 383 to nucleotide 3958;
- (c) the nucleotide sequence of SEQ ID NO:129 from nucleotide 470 to nucleotide 3958;
- (d) the nucleotide sequence of SEQ ID NO:129 from nucleotide 271 to nucleotide 488;
- (e) the nucleotide sequence of the full-length protein coding sequence of clone CO722\_1 deposited with the ATCC under accession number 98271;
- (f) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone CO722\_1 deposited with the ATCC under accession number 98271;
- (g) the nucleotide sequence of a mature protein coding sequence of clone CO722\_1 deposited with the ATCC under accession number 98271;
- (h) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone CO722\_1 deposited with the ATCC under accession number 98271;
- (i) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:130;
- (j) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130, the fragment comprising eight contiguous amino acids of SEQ ID NO:130;
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h); and
- (l) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h), and that has a length that is at least 25% of the length of SEQ ID NO:129.

13. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:130;
- (b) the amino acid sequence of SEQ ID NO:130 from amino acid 1 to amino acid 34;
- (c) a fragment of the amino acid sequence of SEQ ID NO:130, the fragment comprising eight contiguous amino acids of SEQ ID NO:130; and

(d) the amino acid sequence encoded by the cDNA insert of clone CO722\_1 deposited with the ATCC under accession number 98271; the protein being substantially free from other mammalian proteins.

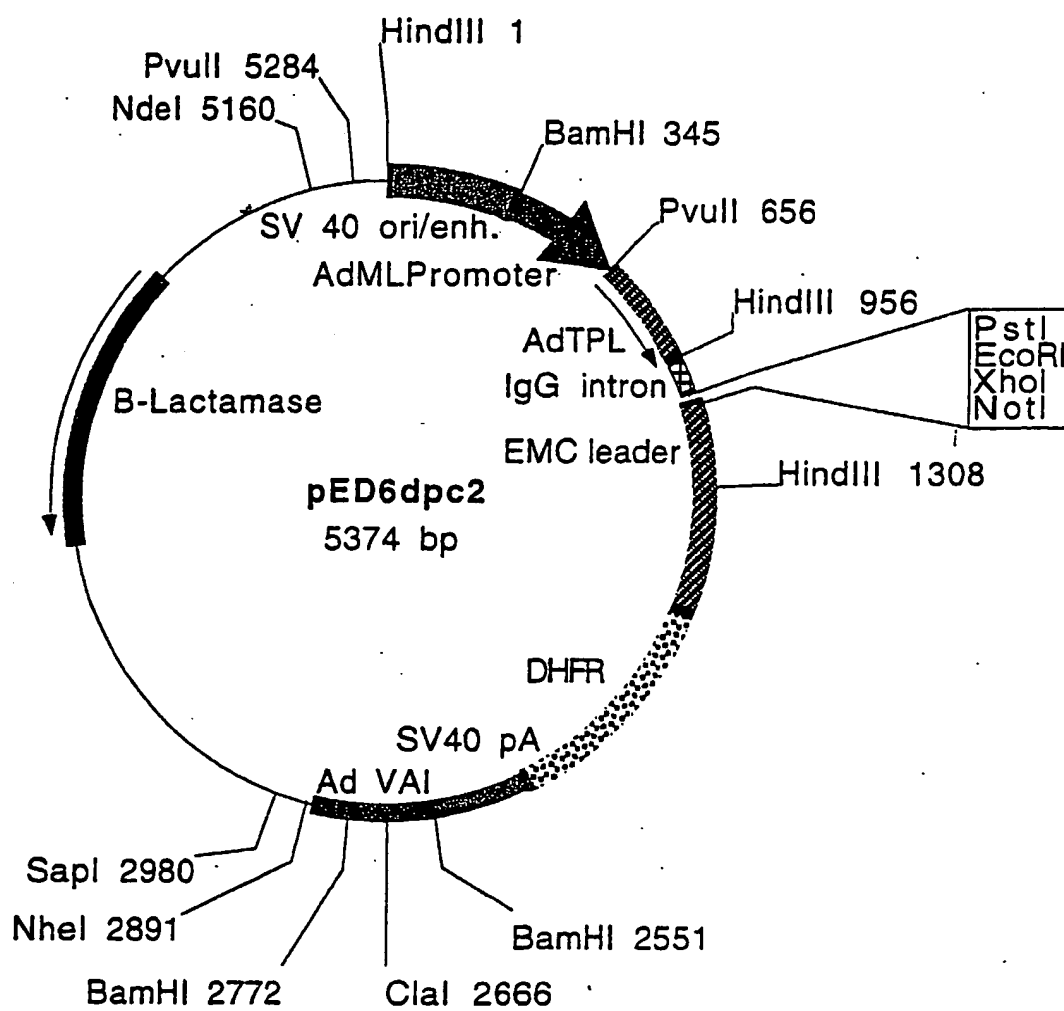


Fig. 1A

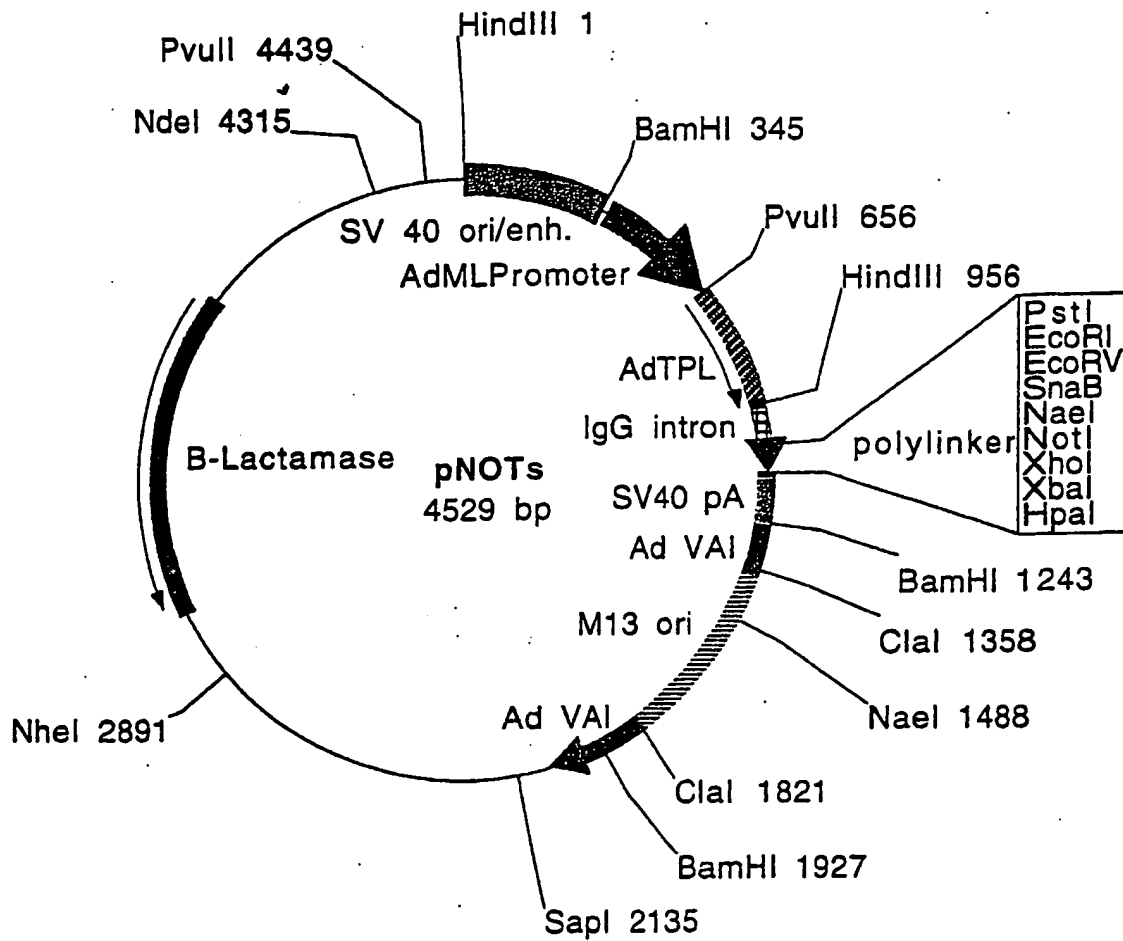


Fig. 1B

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McCoy, John M.  
LaVallie, Edward R.  
Collins-Racie, Lisa A.  
Evans, Cheryl  
Merberg, David  
Treacy, Maurice  
Bowman, Michael R.  
Spaulding, Vikki  
Agostino, Michael J.  
Genetics Institute, Inc.

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Asp Tyr Cys Phe Asp Val Phe Asp Gly Ser Tyr Pro Phe Leu Pro Leu
 65             70             75             80

Val Glu His Ser Gln Pro Xaa Ser Pro Ala Leu Gly Ser Pro
          85             90

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&lt;210&gt; 3

&lt;211&gt; 92

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3

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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 92

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 <212> PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (255)

&lt;400&gt; 5

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Cys Lys Ala Ile Gly Asp Ser Ser Val Pro Ser Glu Cys Pro Gly Thr  
 20 25 30

Leu Asp His Gln Arg Gln Ala Ser Arg Thr Pro Cys Pro Arg Pro Pro  
 35 40 45

Leu Ala Gly Thr Gln Gly Leu Val Thr Asp Thr Arg Ala Ala Pro Leu  
 50 55 60

Thr Pro Ile Gly Thr Pro Leu Pro Ser Ala Ile Pro Ser Gly Tyr Cys  
 65 70 75 80

Ser Gln Asp Gly Gln Thr Gly Arg Gln Pro Leu Pro Pro Tyr Thr Pro  
 85 90 95

Ala Met Met His Arg Ser Asn Gly His Thr Leu Thr Gln Pro Pro Gly  
 100 105 110

Pro Arg Gly Cys Glu Gly Asp Gly Pro Glu His Gly Val Glu Glu Gly  
 115 120 125

Thr Arg Lys Arg Val Ser Leu Pro Gln Trp Pro Pro Pro Ser Arg Ala  
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Lys Trp Ala His Ala Ala Arg Glu Asp Ser Leu Pro Glu Glu Ser Ser  
 145 150 155 160

Ala Pro Asp Phe Ala Asn Leu Lys His Tyr Gln Lys Gln Gln Ser Leu  
 165 170 175

Pro Ser Leu Cys Ser Thr Ser Asp Pro Asp Thr Pro Leu Gly Ala Pro  
 180 185 190

Ser Thr Pro Gly Arg Ile Ser Leu Arg Ile Ser Glu Ser Val Leu Arg  
 195 200 205

Asp Ser Pro Pro Pro His Glu Asp Tyr Glu Asp Glu Val Phe Val Arg  
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Asp Pro His Pro Lys Ala Thr Ser Ser Pro Thr Phe Glu Pro Leu Pro  
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Pro Pro Pro Pro Pro Pro Pro Ser Gln Glu Thr Pro Val Tyr Xaa Met  
 245 250 255

Asp Asp Phe Pro Pro Pro Pro Pro His Thr Val Cys Glu Ala Gln Leu  
 260 265 270

Asp Ser Glu Asp Pro Glu Gly Pro Arg Pro Ser Phe Asn Lys Leu Ser  
 275 280 285

Lys Val Thr Ile Ala Arg Glu Arg His Met Pro Gly Ala Ala His Val  
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 Val Gly Ser Gln Thr Leu Ala Ser Arg Leu Gln Thr Ser Ile Lys Gly  
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 Ser Glu Ala Glu Ser Thr Pro Pro Ser Phe Met Ser Val His Ala Gln  
 325 330 335  
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 340 345 350  
 Leu Ser His Asp Pro Val Ser Gly Thr Gln Gly Leu Glu Lys Lys Val  
 355 360 365  
 Ser Pro Asp Pro Gln Lys Ser Ser Glu Asp Ile Arg Thr Glu Ala Leu  
 370 375 380  
 Ala Lys Glu Ile Val His Gln Asp Lys Ser Leu Ala Asp Ile Leu Asp  
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 420 425 430  
 Ile Gln Arg Thr Val Ser Ser Ser Gly Cys Glu Gly Lys Arg Asn Glu  
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 485 490 495  
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 500 505 510  
 Ala Lys Gly Ser Leu Leu Thr Asp Ile Lys Leu Asn Asn Ala Leu Gly  
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 Glu Glu Val Glu Ala Leu Ile Ser Glu Leu Cys Lys Pro Asn Glu Phe  
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 Asp Lys Tyr Arg Met Phe Ile Gly Asp Leu Asp Lys Val Val Asn Leu  
 545 550 555 560  
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 565 570 575  
 Gly Leu Gly Glu Asp Ala Ser Asn Glu Glu Arg Ser Ser Leu Tyr Glu  
 580 585 590  
 Lys Arg Lys Ile Leu Ala Gly Gln His Glu Asp Ala Arg Glu Leu Lys  
 595 600 605

Glu Asn Leu Asp Arg Arg Glu Arg Val Val Leu Gly Ile Leu Ala Asn  
 610 615 620  
 Tyr Leu Ser Glu Glu Gln Leu Gln Asp Tyr Gln His Phe Val Lys Met  
 625 630 635 640  
 Lys Ser Thr Leu Leu Ile Glu Gln Arg Lys Leu Asp Asp Lys Ile Lys  
 645 650 655  
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 660 665 670  
 Phe Ile Pro Lys Ala Gly Ala Leu Ala Leu Pro Pro Asn Leu Thr Ser  
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 <222> (4)

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<400> 7

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<211> 62

<212> PRT

<213> Homo sapiens

<400> 8

Thr Ser Phe Val Arg Ala Ile Val Val Ser Lys Leu Leu Gly Lys Thr  
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Lys Lys Lys Asn Pro Lys Glu Glu Gly Phe Ser Pro Phe Pro Val Trp  
 20 25 30

Phe Ile Thr Ala Phe Cys Phe Phe Phe Gly Thr Ala Phe Tyr Val Ser  
 35 40 45

Phe His Ser Ala Ile Thr Glu Pro Val Pro Gly Gly Asn Gln  
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<211> 267

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (21)

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<211> 2178

<212> DNA

<213> Homo sapiens

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&lt;210&gt; 11

&lt;211&gt; 487

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 11

```

Met Ser Leu Pro Pro Ile Arg Leu Pro Ser Pro Tyr Gly Ser Asp Arg
  1             5             10             15

```

```

Leu Val Gln Leu Ala Ala Arg Leu Arg Pro Ala Leu Cys Asp Thr Leu
      20             25             30

```

```

Ile Thr Val Gly Ser Gln Glu Phe Pro Ala His Ser Leu Val Leu Ala
      35             40             45

```

```

Gly Val Ser Gln Gln Leu Gly Arg Arg Gly Gln Trp Ala Leu Gly Glu
      50             55             60

```

```

Gly Ile Ser Pro Ser Thr Phe Ala Gln Leu Leu Asn Phe Val Tyr Gly
      65             70             75             80

```

```

Glu Ser Val Glu Leu Gln Pro Gly Glu Leu Arg Pro Leu Gln Glu Ala
      85             90             95

```

```

Ala Arg Ala Leu Gly Val Gln Ser Leu Glu Glu Ala Cys Trp Arg Ala
      100            105            110

```

```

Arg Gly Asp Arg Ala Lys Lys Pro Asp Pro Gly Leu Lys Lys His Gln
      115            120            125

```

```

Glu Glu Pro Glu Lys Pro Ser Arg Asn Pro Glu Arg Glu Leu Gly Asp
      130            135            140

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Pr  Gly Glu Lys Gln Lys Pro Glu Gln Val Ser Arg Thr Gly Gly Arg
145                      150                      155                      160

Glu Gln Glu Met Leu His Lys His Ser Pro Pro Arg Gly Arg Pro Glu
                      165                      170                      175

Met Ala Gly Ala Thr Gln Glu Ala Gln Gln Glu Gln Thr Arg Ser Lys
                      180                      185                      190

Glu Lys Arg Leu Gln Ala Pro Val Gly Gln Arg Gly Ala Asp Gly Lys
                      195                      200                      205

His Gly Val Leu Thr Trp Leu Arg Glu Asn Pro Gly Gly Ser Glu Glu
210                      215                      220

Ser Leu Arg Lys Leu Pro Gly Pro Leu Pro Pro Ala Gly Ser Leu Gln
225                      230                      235                      240

Thr Ser Val Thr Pro Arg Pro Ser Trp Ala Glu Ala Pro Trp Leu Val
                      245                      250                      255

Gly Gly Gln Pro Ala Leu Trp Ser Ile Leu Leu Met Pro Pro Arg Tyr
                      260                      265                      270

Gly Ile Pro Phe Tyr His Ser Thr Pro Thr Thr Gly Ala Trp Gln Glu
                      275                      280                      285

Val Trp Arg Glu Gln Arg Ile Pro Leu Ser Leu Asn Ala Pro Lys Gly
290                      295                      300

Leu Trp Ser Gln Asn Gln Leu Ala Ser Ser Ser Pro Thr Pro Gly Ser
305                      310                      315                      320

Leu Pro Gln Gly Pro Ala Gln Leu Ser Pro Gly Glu Met Glu Glu Ser
                      325                      330                      335

Asp Gln Gly His Thr Gly Ala Leu Ala Thr Cys Ala Gly His Glu Asp
                      340                      345                      350

Lys Ala Gly Cys Pro Pro Arg Pro His Pro Pro Pro Ala Pro Pro Ala
                      355                      360                      365

Arg Ser Arg Pro Tyr Ala Cys Ser Val Cys Gly Lys Arg Phe Ser Leu
370                      375                      380

Lys His Gln Met Glu Thr His Tyr Arg Val His Thr Gly Glu Lys Pro
385                      390                      395                      400

Phe Ser Cys Ser Leu Cys Pro Gln Arg Ser Arg Asp Phe Ser Ala Met
                      405                      410                      415

Thr Lys His Leu Arg Thr His Gly Ala Ala Pro Tyr Arg Cys Ser Leu
420                      425                      430

Cys Gly Ala Gly Cys Pro Ser Leu Ala Ser Met Gln Ala His Met Arg
435                      440                      445

Gly His Ser Pro Ser Gln Leu Pro Pro Gly Trp Thr Ile Arg Ser Thr
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Phe Leu Tyr Ser Ser Ser Arg Pro Ser Arg Pro Ser Thr Ser Pro Cys  
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Cys Pro Ser Ser Ser Thr Thr  
 485

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 <212> DNA  
 <213> Homo sapiens

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<210> 13  
 <211> 763  
 <212> PRT  
 <213> Homo sapiens



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 Leu Trp Asp Tyr Ile Asp Gly Ile Leu Ile Lys Thr Phe Ile Val Gly  
 20 25 30  
 Cys Lys Leu His Ala Leu Phe Thr Leu Ala Gln Ala Glu Asp Ser Val  
 35 40 45  
 Phe Val Ile Val Asn Lys Glu Lys Pro Asp Ile Phe Gln Leu Val Ser  
 50 55 60  
 Val Lys Leu Pro Lys Ser Ser Ser Gln Glu Val Glu Ala Lys Glu Leu  
 65 70 75 80  
 Ser Phe Val Leu Asp Tyr Ile Asn Gln Ser Pro Lys Cys Ile Ala Phe  
 85 90 95  
 Gly Asn Glu Gly Val Tyr Val Ala Ala Val Arg Glu Phe Tyr Leu Ser  
 100 105 110  
 Val Tyr Phe Phe Lys Lys Lys Thr Thr Ser Arg Phe Thr Leu Ser Ser  
 115 120 125  
 Ser Arg Asn Lys Lys His Ala Lys Asn Asn Phe Thr Cys Val Ala Cys  
 130 135 140  
 His Pro Thr Glu Asp Cys Ile Ala Ser Gly His Met Asp Gly Lys Ile  
 145 150 155 160  
 Arg Leu Trp Arg Asn Phe Tyr Asp Asp Lys Lys Tyr Thr Tyr Thr Cys  
 165 170 175  
 Leu His Trp His His Asp Met Val Met Asp Leu Ala Phe Ser Val Thr  
 180 185 190  
 Gly Thr Ser Leu Leu Ser Gly Gly Arg Glu Ser Val Leu Val Glu Trp  
 195 200 205  
 Arg Asp Ala Thr Glu Lys Asn Lys Glu Phe Leu Pro Arg Leu Gly Ala  
 210 215 220  
 Thr Ile Glu His Ile Ser Val Ser Pro Ala Gly Asp Leu Phe Cys Thr  
 225 230 235 240  
 Ser His Ser Asp Asn Lys Ile Ile Ile Ile His Arg Asn Leu Glu Ala  
 245 250 255  
 Ser Ala Val Ile Gln Gly Leu Val Lys Asp Arg Ser Ile Phe Thr Gly  
 260 265 270  
 Leu Met Ile Asp Pro Arg Thr Lys Ala Leu Val Leu Asn Gly Lys Pro  
 275 280 285  
 Gly His Leu Gln Phe Tyr Ser Leu Gln Ser Asp Lys Gln Leu Tyr Asn  
 290 295 300  
 Leu Asp Ile Ile Gln Gln Glu Tyr Ile Asn Asp Tyr Gly Leu Ile Gln  
 305 310 315 320

Ile Glu Leu Thr Lys Ala Ala Phe Gly Cys Phe Gly Asn Trp Leu Ala  
 325 330 335  
 Thr Val Glu Gln Arg Gln Glu Lys Glu Thr Glu Leu Glu Leu Gln Met  
 340 345 350  
 Lys Leu Trp Met Tyr Asn Lys Lys Thr Gln Gly Phe Ile Leu Asn Thr  
 355 360 365  
 Lys Ile Asn Met Pro His Glu Asp Cys Ile Thr Ala Leu Cys Phe Cys  
 370 375 380  
 Asn Ala Glu Lys Ser Glu Gln Pro Thr Leu Val Thr Ala Ser Lys Asp  
 385 390 395 400  
 Gly Tyr Phe Lys Val Trp Ile Leu Thr Asp Asp Ser Asp Ile Tyr Lys  
 405 410 415  
 Lys Ala Val Gly Trp Thr Cys Asp Phe Val Gly Ser Tyr His Lys Tyr  
 420 425 430  
 Gln Ala Thr Asn Cys Cys Phe Ser Glu Asp Gly Ser Leu Leu Ala Val  
 435 440 445  
 Ser Phe Glu Glu Ile Val Thr Ile Trp Asp Ser Val Thr Trp Glu Leu  
 450 455 460  
 Lys Cys Thr Phe Cys Gln Arg Ala Gly Lys Ile Arg His Leu Cys Phe  
 465 470 475 480  
 Gly Arg Leu Thr Cys Ser Lys Tyr Leu Leu Gly Ala Thr Glu Asn Gly  
 485 490 495  
 Ile Leu Cys Cys Trp Asn Leu Leu Ser Cys Ala Leu Glu Trp Asn Ala  
 500 505 510  
 Lys Leu Asn Val Arg Val Met Glu Pro Asp Pro Asn Ser Glu Asn Ile  
 515 520 525  
 Ala Ala Ile Ser Gln Ser Ser Val Gly Ser Asp Leu Phe Val Phe Lys  
 530 535 540  
 Pro Ser Glu Pro Arg Pro Leu Tyr Ile Gln Lys Gly Ile Ser Arg Glu  
 545 550 555 560  
 Lys Val Gln Trp Gly Val Phe Val Pro Arg Asp Val Pro Glu Ser Phe  
 565 570 575  
 Thr Ser Glu Ala Tyr Gln Trp Leu Asn Arg Ser Gln Phe Tyr Phe Leu  
 580 585 590  
 Thr Lys Ser Gln Ser Leu Leu Thr Phe Ser Thr Lys Ser Pro Glu Glu  
 595 600 605  
 Lys Leu Thr Pro Thr Ser Lys Gln Leu Leu Ala Glu Glu Ser Leu Pro  
 610 615 620  
 Thr Thr Pro Phe Tyr Phe Ile Leu Gly Lys His Arg Gln Gln Gln Asp  
 625 630 635 640

Glu Lys Leu Asn Glu Thr Leu Glu Asn Glu Leu Val Gln Leu Pro Leu  
                     645                    650                    655  
 Thr Glu Asn Ile Pro Ala Ile Ser Glu Leu Leu His Thr Pro Ala His  
                     660                    665                    670  
 Val Leu Pro Ser Ala Ala Phe Leu Cys Ser Met Phe Val Asn Ser Leu  
                     675                    680                    685  
 Leu Leu Ser Lys Glu Thr Lys Ser Ala Lys Glu Ile Pro Glu Asp Val  
                     690                    695                    700  
 Asp Met Glu Glu Glu Lys Glu Ser Glu Asp Ser Asp Glu Glu Asn Asp  
 705                    710                    715                    720  
 Phe Thr Glu Lys Val Gln Asp Thr Ser Asn Thr Gly Leu Gly Glu Asp  
                     725                    730                    735  
 Ile Ile His Gln Leu Ser Lys Ser Glu Glu Lys Glu Leu Arg Lys Phe  
                     740                    745                    750  
 Arg Lys Ile Asp Tyr Ser Trp Ile Ala Ala Leu  
                     755                    760

<210> 14  
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 <212> DNA  
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ngcgtcatgg atggaat 137

<210> 15  
<211> 539  
<212> DNA  
<213> Homo sapiens

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ccaccagccc agggaatgcc tctaccagtt gtcagcgaga ggcttacaca gcatcttaaa 180  
taaaagggat tattgaacca agaggccagg gactgatgga aatgccacc ttgctggctc 240  
attgaaaaag tttggcaagg ttgtcaggag acatgaatta gatgggcttg ggtcttgtgc 300  
cctttgctaa accaagtgtc gtattgggaa agagacgggg agagaagtgt tggagatgct 360  
ctttagtcag gcctgagtca cttgccaac cctggagttg gagttgggga tggagccagg 420  
atctccaaac cacatgcccc tagagtttca gggaaaatat ggattgtgaa ttgaagatgg 480  
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<210> 16  
<211> 27  
<212> PRT  
<213> Homo sapiens

<400> 16  
Met Asp Cys Glu Leu Lys Met Gly Gly Asp Val Arg Gln Thr Arg Thr  
1 5 10 15

Glu Asn Pro Ser Ser Ser Cys Asp Leu Ala Val  
20 25

<210> 17  
 <211> 99  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 antnatccca tggggagcag cacnttatga aaaaaaaaaa 99

<210> 18  
 <211> 2608  
 <212> DNA  
 <213> Homo sapiens

<400> 18  
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 agtccatttt cttatcccta aaagagggct gagaagctca cccctacctt tgaaggttgt 240  
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 catgtgccag ggccaagagg gccttcagcg tcgcctccag tccagccctg tcctcgtatt 660  
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 cagcagtcgc tgcccccgga atcccagcaa gtgcgggtggg agaagcagca gccaaccccc 1380  
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa

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2608

&lt;210&gt; 19

&lt;211&gt; 236

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 19

```

Met Glu Ser Arg Pro Pro Ala Gln Thr Ser Leu Pro Ala Ser Ser Gly
  1             5             10             15

```

```

Leu Asp Asp Leu Asp Leu Leu Gly Lys Thr Leu Leu Gln Gln Ser Leu
      20             25             30

```

```

Pro Pro Glu Ser Gln Gln Val Arg Trp Glu Lys Gln Gln Pro Thr Pro
      35             40             45

```

```

Arg Leu Thr Leu Arg Asp Leu Gln Asn Lys Ser Ser Ser Cys Ser Ser
      50             55             60

```

```

Pro Ser Ser Ser Ala Thr Ser Leu Leu His Thr Val Ser Pro Glu Pro
      65             70             75             80

```

```

Pro Arg Pro Pro Gln Gln Pro Val Pro Thr Glu Leu Ser Leu Ala Ser
      85             90             95

```

```

Ile Thr Val Pro Leu Glu Ser Ile Lys Pro Ser Asn Ile Leu Pro Val
      100            105            110

```

```

Thr Val Tyr Asp Gln His Gly Phe Arg Ile Leu Phe His Phe Ala Arg
      115            120            125

```

```

Asp Pro Leu Pro Gly Arg Ser Asp Val Leu Val Val Val Ser Met
      130            135            140

```

```

Leu Ser Thr Ala Pro Gln Pro Ile Arg Asn Ile Val Phe Gln Ser Ala
      145            150            155            160

```

```

Val Pro Lys Val Met Lys Val Lys Leu Gln Pro Pro Ser Gly Thr Glu
      165            170            175

```

Leu Pro Ala Phe Asn Pro Ile Val His Pro Ser Ala Ile Thr Gln Val  
 180 185 190

Leu Leu Leu Ala Asn Pro Gln Lys Glu Lys Val Arg Leu Arg Tyr Lys  
 195 200 205

Leu Thr Phe Thr Met Gly Asp Gln Thr Tyr Asn Glu Met Gly Asp Val  
 210 215 220

Asp Gln Phe Pro Pro Pro Glu Thr Trp Gly Ser Leu  
 225 230 235

<210> 20

<211> 328

<212> DNA

<213> Homo sapiens

<400> 20

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 agagaatcca aacaatcaca ccctccagta ctggaaggac cacaacatcg tgacagcaga 180  
 agtccactgg gctaacctga ctgtcagtga atgccaggag atgcatggag agttcatggg 240  
 atctgcgtgc ggccatcatg gacctacac tctgatgtc ctcttttggt cctgtattct 300  
 ctttttcacc accttcattc tctcaagc 328

<210> 21

<211> 87

<212> PRT

<213> Homo sapiens

<400> 21

Met His Ser Gln Leu Asp His Leu Ser Leu Tyr Tyr Cys Arg Cys Thr  
 1 5 10 15

Leu Pro Glu Asn Pro Asn Asn His Thr Leu Gln Tyr Trp Lys Asp His  
 20 25 30

Asn Ile Val Thr Ala Glu Val His Trp Ala Asn Leu Thr Val Ser Glu  
 35 40 45

Cys Gln Glu Met His Gly Glu Phe Met Gly Ser Ala Cys Gly His His  
 50 55 60

Gly Pro Tyr Thr Pro Asp Val Leu Phe Trp Ser Cys Ile Leu Phe Phe  
 65 70 75 80

Thr Thr Phe Ile Leu Ser Ser  
 85

<210> 22

<211> 326

<212> DNA

<213> Homo sapiens

<220>

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<220>  
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 <222> (82)

<220>  
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<220>  
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 <222> (129)

<400> 22  
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 tgggaataana cgtggattgg gtcaactgat tatcagcttg ttaggagtcc tctgtgtgag 180  
 acatgggtggg ataattgtga agttctcact gtatgtggat gttcatgtga aagatagtac 240  
 tttcttcccg taaatatctt ttgatttcca tttgtatgga atcccaatga atgtatcttt 300  
 ggaaaacaaa aaaaaaaaaa aaaaaa 326

<210> 23  
 <211> 194  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (55)

<220>  
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 ggcttttagca canaaaggtc tttatgtcac tgaccaggaa aaattggtaa ctgaacgana 120  
 tctccncaag aaaccntac agatgagtgac acatttgggc catgatcgat accncatgat 180  
 ggcttatact gtat 194

<210> 24



<211> 396  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (139)

<400> 24  
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 ctttggctga tagcctgtat aatctgcagc tgattcaaga attttgccaa gaatacttga 120  
 accagtgttg ccatttcant ctggaagata tgctctatgc tgcttcatcc ataaagagta 180  
 attatttggg gttcatggcg gaactgttct ggtgggttga agtgggtgaag ccgtcttttg 240  
 tacagcctcg tgttggtcgt ccacaaggag ctgaacctgt aaaagatatg ccttcaattc 300  
 ctgtcttgaa tgctgccaaa agaaatgtct tagatagtag ttctgacttc ccttcaagtg 360  
 ggggaaggagc tacatttaca cagtctcacc tcgagg 396

<210> 25  
 <211> 113  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (28)

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 20 25 30  
 Leu Tyr Ala Ala Ser Ser Ile Lys Ser Asn Tyr Leu Val Phe Met Ala  
 35 40 45  
 Glu Leu Phe Trp Trp Phe Glu Val Val Lys Pro Ser Phe Val Gln Pro  
 50 55 60  
 Arg Val Val Arg Pro Gln Gly Ala Glu Pro Val Lys Asp Met Pro Ser  
 65 70 75 80  
 Ile Pro Val Leu Asn Ala Ala Lys Arg Asn Val Leu Asp Ser Ser Ser  
 85 90 95  
 Asp Phe Pro Ser Ser Gly Glu Gly Ala Thr Phe Thr Gln Ser His Leu  
 100 105 110  
 Glu

<210> 26  
 <211> 336  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (87)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (123)

&lt;400&gt; 26

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aaatgatatg gcaatgaaac gggcagnttt gttggagaaa agattaagaa gggaaaagga 120
aantcagctc cggaacaac agttggaagc agaaatggag cataagaagg aggaacaag 180
gcgtaaaact gaggaagaac gtcagaagaa agaagatgag agagcacgca gagaatttat 240
taggcaagaa tatatgagc ggaacaact gaaactaat gaagatatgg atacagtaat 300
taaaccccgct cctcaagtag taaaaaaaaa aaaaaa 336

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&lt;210&gt; 27

&lt;211&gt; 917

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 27

```

cacctggatt atctcagtag tttcccaact ggtttccttg tttccattct tgccctcttc 60
tgtctactct caatataaca gctagaacaa tccttttaca atggaattca gatcatgttt 120
acccctctgt tcaaattctc cagtgcacttt ccagttttta catgatctgg ctccctactac 180
ctgtctcact gtgtttccta ctactctect gccctttctc ctcttaataa acactgggct 240
catgggtgtt cctttaacat gccaggcatg cttgaccctg tcctgtctca gggccctgct 300
gttccctctg cctggaacat tcttcccata gtgtctgcat ggctcgtctc ctactgctt 360
tggattgctg ctcaaaaagtc accttatcaa aggcctttcc caaagggtta aaaatcattc 420
tactataaag acacatgcat acatatgttt attgcagcac tattcacaat aacaaagact 480
tggaaccaac ccaaatgccc atcaatgata gactggataa agaaaatatg gcacgtaagc 540
accatggaat actatgcagc cataaaaaag aatgagttca tgtcctttgc agggacatgg 600
atgaagctgg aaaccattat tctcagcaaa ctaacacagg aacagaaaac caaacaccgc 660
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atcacacacc agggcctgtc ggggggtgag aggcaaggga agtgatagca ttaagagaaa 780
tacctaattg agattatggg ttgatggggg cagcaaacca ccatggcaca tgtgtacct 840
tgtaacaaac ctgcacattc tgacatatata tcccagaact taaagtataa ttaaagaaaa 900
agaaaaaaaa aaaaaa 917

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&lt;210&gt; 28

&lt;211&gt; 76

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 28

```

Met Glu Phe Arg Ser Cys Leu Pro Leu Cys Ser Asn Ser Pro Val Thr
  1              5              10              15

Phe Gln Phe Leu His Asp Leu Ala Pro Thr Thr Cys Leu Thr Val Phe
      20              25              30

Pro Thr Thr Leu Leu Pro Phe Leu Leu Leu Ile Asn Thr Gly Leu Met
      35              40              45

Val Phe Pro Leu Thr Cys Gln Ala Cys Leu Thr Leu Ser Cys Leu Arg
      50              55              60

Ala Leu Leu Phe Pro Leu Pro Gly Thr Phe Phe Pro
      65              70              75

```

&lt;210&gt; 29

&lt;211&gt; 351

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 29

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ggcttttgacc gctatcgcca ggagtggatg gactatggct gtgcacagga ggcagagggc 60
aggatgtgcg aggacttcca ggatgaggac cagactcag cctcccctga cacttccttc 120
agcccctatg atggagacct caccamtacc tcctcctccc tcttcacga cagcctcacc 180
acagaagatg acaccaagtt gaatccctat gcaggaggag acggccttca gaacaacctg 240
tcccccaaga caaagggcac tcctgtgcac ctgggcacca tcgtgggcat cgtgctggca 300
gtcctcctcg tggcggccat catcctggct ggaatttaca tcaatggcca c 351

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&lt;210&gt; 30

&lt;211&gt; 108

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (40)

&lt;400&gt; 30

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Met Asp Tyr Gly Cys Ala Gln Glu Ala Glu Gly Arg Met Cys Glu Asp
 1             5             10             15
Phe Gln Asp Glu Asp His Asp Ser Ala Ser Pro Asp Thr Ser Phe Ser
      20             25             30
Pro Tyr Asp Gly Asp Leu Thr Xaa Thr Ser Ser Ser Leu Phe Ile Asp
      35             40             45
Ser Leu Thr Thr Glu Asp Asp Thr Lys Leu Asn Pro Tyr Ala Gly Gly
      50             55             60
Asp Gly Leu Gln Asn Asn Leu Ser Pro Lys Thr Lys Gly Thr Pro Val
      65             70             75             80
His Leu Gly Thr Ile Val Gly Ile Val Leu Ala Val Leu Leu Val Ala
      85             90             95
Ala Ile Ile Leu Ala Gly Ile Tyr Ile Asn Gly His
      100             105

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&lt;210&gt; 31

&lt;211&gt; 179

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (24)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (33)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (56)

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 <222> (99)

<220>  
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 <222> (117)

<220>  
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 <222> (137)

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 ataaagtccc tttctnngct ccaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 179

<210> 32  
 <211> 3906  
 <212> DNA  
 <213> Homo sapiens

<400> 32  
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```

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aaaaaa 3906

```

&lt;210&gt; 33

&lt;211&gt; 286

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 33

```

Met Lys Cys Ser Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn
  1             5             10             15

```

```

Tyr Thr Leu Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys
      20             25             30

```

```

Glu Asn Ile Phe Arg Glu Gly Gln Tyr Leu Gly Cys Ser Phe Asp Leu
      35             40             45

```

```

Thr Lys Val Lys Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met
      50             55             60

```

```

Val Lys Asp Asn Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro
      65             70             75             80

```

```

Leu Thr Ser Arg Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser

```

85	90	95
Phe His Asn Asp Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn Phe		
100	105	110
Ile Ser Arg Cys Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr		
115	120	125
Glu Thr His Asn Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro		
130	135	140
Glu Phe Glu Arg Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly		
145	150	155
Val Leu Pro Asp Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn		
165	170	175
Lys Leu Cys Tyr Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu		
180	185	190
Met Ser Ile Gly Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu		
195	200	205
Leu Ile Val Pro Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Leu		
210	215	220
Tyr Leu Lys Arg Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro		
225	230	235
Gly Lys Ile Phe Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu		
245	250	255
His Trp Lys Lys Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr		
260	265	270
Asp Ser Val Val Leu Ile Glu Asn Leu Lys Lys Ala Ser Gln		
275	280	285

&lt;210&gt; 34

&lt;211&gt; 1605

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 34

```

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aagatgttta cagagaccct tctccctgtg cagttaggag tgtaaggcaa gagagcccct 180
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gcattcctcg acgttgctgg tagtgctgtc catcaagaaa gattatggtt cccaggaaga 840
cttcactcaa gtgtggaaca ccaccatgaa agggctcaag tgctgtggct tcaccaacta 900

```

```

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```

&lt;210&gt; 35

&lt;211&gt; 241

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 35

```

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
  1              5              10              15

```

```

Leu Ile Phe Leu Cys Gly Ala Ala Leu Ala Val Gly Ile Trp Val
      20              25              30

```

```

Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
      35              40              45

```

```

Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly
      50              55              60

```

```

Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr
      65              70              75              80

```

```

Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile
      85              90              95

```

```

Phe Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr
      100             105             110

```

```

Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys
      115             120             125

```

```

Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met
      130             135             140

```

```

Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp
      145             150             155             160

```

```

Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn
      165             170             175

```

```

Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala
      180             185             190

```

```

His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile
      195             200             205

```

```

Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly
      210             215             220

```

Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu  
 225 230 235 240

Gln

<210> 36  
 <211> 377  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (346)

<400> 36  
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 ccacgtggcg cgggccaccc cgggctcaga ccaggcagtg ctagccctgt cccctgagta 300  
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 ctgtgtgcct ctgctgc 377

<210> 37  
 <211> 106  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (96)

<400> 37  
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 Arg Leu Leu Leu Ala Ala Asn Val Ala Thr Leu Gly Leu Leu Met Ala  
 20 25 30  
 Arg Leu Leu Ser Thr Ser Pro Ala Leu Gln Gly Thr Pro Ala Ser Arg  
 35 40 45  
 Gly Phe Phe Ala Ala Ala Ile Leu Phe Leu Ser Gln Ser His Val Ala  
 50 55 60  
 Arg Ala Thr Pro Gly Ser Asp Gln Ala Val Leu Ala Leu Ser Pro Glu  
 65 70 75 80  
 Tyr Glu Gly Ile Trp Ala Asp Leu Gln Glu Leu Trp Phe Leu Gly Xaa  
 85 90 95  
 Gln Ala Phe Thr Gly Cys Val Pro Leu Leu  
 100 105

<210> 38  
 <211> 245



&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (3)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (17)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (34)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (46)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (65)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (71)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (142)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (214)

&lt;400&gt; 38

```

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accnnggggg nccacacaca cacacacaca cacacacaca cacacacaca 120
catttttgat cccttgcttc cntccccagc tgcgttctgt gatcgccaag ttcaaagctg 180
tgcacatgtg gacactcaat aaatgttcat tggngacaaa aaaaaaaaaa aaaaaaaaaa 240
aaaaa                                           245

```

&lt;210&gt; 39

&lt;211&gt; 2384

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 39

```

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```

```

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```

&lt;210&gt; 40

&lt;211&gt; 614

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (607)

&lt;400&gt; 40

```

Met Ile Asn Lys Thr Gly Phe Lys Phe Ser Ala Glu Lys Pro Val Ile
  1              5              10              15

```

```

Glu Val Pro Ser Met Thr Ile Leu Asp Lys Lys Asp Gly Glu Gln Ala
          20              25              30

```

```

Lys Ala Leu Phe Glu Lys Val Arg Lys Phe Arg Ala His Val Glu Asp
    35              40              45

```

```

Ser Asp Leu Ile Tyr Lys Leu Tyr Val Val Gln Thr Val Ile Lys Thr
    50              55              60

```

```

Ala Lys Phe Ile Phe Ile Leu Cys Tyr Thr Ala Asn Phe Val Asn Ala
    65              70              75              80

```

```

Ile Ser Phe Glu His Val Cys Lys Pro Lys Val Glu His Leu Ile Gly
          85              90              95

```

```

Tyr Glu Val Phe Glu Cys Thr His Asn Met Ala Tyr Met Leu Lys Lys
    100              105              110

```

Leu Leu Ile Ser Tyr Ile Ser Ile Ile Cys Val Tyr Gly Phe Ile Cys  
 115 120 125  
 Leu Tyr Thr Leu Phe Trp Leu Phe Arg Ile Pro Leu Lys Glu Tyr Ser  
 130 135 140  
 Phe Glu Lys Val Arg Glu Glu Ser Ser Phe Ser Asp Ile Pro Asp Val  
 145 150 155 160  
 Lys Asn Asp Phe Ala Phe Leu Leu His Met Val Asp Gln Tyr Asp Gln  
 165 170 175  
 Leu Tyr Ser Lys Arg Phe Gly Val Phe Leu Ser Glu Val Ser Glu Asn  
 180 185 190  
 Lys Leu Arg Glu Ile Ser Leu Asn His Glu Trp Thr Phe Glu Lys Leu  
 195 200 205  
 Arg Gln His Ile Ser Arg Asn Ala Gln Asp Lys Gln Glu Leu His Leu  
 210 215 220  
 Phe Met Leu Ser Gly Val Pro Asp Ala Val Phe Asp Leu Thr Asp Leu  
 225 230 235 240  
 Asp Val Leu Lys Leu Glu Leu Ile Pro Glu Ala Lys Ile Pro Ala Lys  
 245 250 255  
 Ile Ser Gln Met Thr Asn Leu Gln Glu Leu His Leu Cys His Cys Pro  
 260 265 270  
 Ala Lys Val Glu Gln Thr Ala Phe Ser Phe Leu Arg Asp His Leu Arg  
 275 280 285  
 Cys Leu His Val Lys Phe Thr Asp Val Ala Glu Ile Pro Ala Trp Val  
 290 295 300  
 Tyr Leu Leu Lys Asn Leu Arg Glu Leu Tyr Leu Ile Gly Asn Leu Asn  
 305 310 315 320  
 Ser Glu Asn Asn Lys Met Ile Gly Leu Glu Ser Leu Arg Glu Leu Arg  
 325 330 335  
 His Leu Lys Ile Leu His Val Lys Ser Asn Leu Thr Lys Val Pro Ser  
 340 345 350  
 Asn Ile Thr Asp Val Ala Pro His Leu Thr Lys Leu Val Ile His Asn  
 355 360 365  
 Asp Gly Thr Lys Leu Leu Val Leu Asn Ser Leu Lys Lys Met Met Asn  
 370 375 380  
 Val Ala Glu Leu Glu Leu Gln Asn Cys Glu Leu Glu Arg Ile Pro His  
 385 390 395 400  
 Ala Ile Phe Ser Leu Ser Asn Leu Gln Glu Leu Asp Leu Lys Ser Asn  
 405 410 415  
 Asn Ile Arg Thr Ile Glu Glu Ile Ile Ser Phe Gln His Leu Lys Arg  
 420 425 430

Leu Thr Cys Leu Lys Leu Trp His Asn Lys Ile Val Thr Ile Pro Pro  
 435 440 445  
 Ser Ile Thr His Val Lys Asn Leu Glu Ser Leu Tyr Phe Ser Asn Asn  
 450 455 460  
 Lys Leu Glu Ser Leu Pro Val Ala Val Phe Ser Leu Gln Lys Leu Arg  
 465 470 475 480  
 Cys Leu Asp Val Ser Tyr Asn Asn Ile Ser Met Ile Pro Ile Glu Ile  
 485 490 495  
 Gly Leu Leu Gln Asn Leu Gln His Leu His Ile Thr Gly Asn Lys Val  
 500 505 510  
 Asp Ile Leu Pro Lys Gln Leu Phe Lys Cys Ile Lys Leu Arg Thr Leu  
 515 520 525  
 Asn Leu Gly Gln Asn Cys Ile Thr Ser Leu Pro Glu Lys Val Gly Gln  
 530 535 540  
 Leu Ser Gln Leu Thr Gln Leu Glu Leu Lys Gly Asn Cys Leu Asp Arg  
 545 550 555 560  
 Leu Pro Ala Gln Leu Gly Gln Cys Arg Met Leu Lys Lys Ser Gly Leu  
 565 570 575  
 Val Val Glu Asp His Leu Phe Asp Thr Leu Pro Leu Glu Val Lys Glu  
 580 585 590  
 Ala Leu Asn Gln Asp Ile Asn Ile Pro Phe Ala Asn Gly Ile Xaa Thr  
 595 600 605  
 Lys Ile Ile Tyr Ala Gln  
 610  
 <210> 41  
 <211> 2386  
 <212> DNA  
 <213> Homo sapiens  
 <400> 41  
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 cagatttagt acaggaagca tgtgaaagt aattgaatga agttactggt acaaagattg 180  
 cttatgaaac aaaaatggac ttggttcaaa catcagaagt tatgcaagag tcactctatc 240  
 ctgcagcaca gctttgccca tcatttgaag agtcagaagc tactccttca ccagttttgc 300  
 ctgacattgt tatggaagca ccattgaatt ctgcagttcc tagtgctggt gcttccgtga 360  
 tacagcccag ctcatcacca ttagaagctt cttcagttaa ttatgaaagc ataaaacatg 420  
 agcctgaaaa cccccacca tatgaagagg ccattgagtg atcactaaaa aaagtatcag 480  
 gaataaagga agaaattaaa gagcctgaaa atattaatgc agctcttcaa gaaacagaag 540  
 ctcccttat atctattgca tgtgatttaa ttaaagaac aaagctttct gctgaaccag 600  
 ctccggattt ctctgattat tcagaaatgg caaaagtga acagccagt cctgatcatt 660  
 ctgagctagt tgaagattcc tcacctgatt ctgaaccagt tgacttattt agtgatgatt 720  
 caatacctga cgttccacaa aaacaagatg aaactgtgat gcttgtgaaa gaaagtctca 780  
 ctgagacttc atttgagtca atgatagaat atgaaaataa ggaaaaactc agtgctttgc 840  
 cacctgaggg aggaaagcca tatttggaat cttttaagct cagtttagat aacacaaaag 900  
 ataccctggt acctgatgaa gtttcaacat tgagcaaaaa ggagaaaatt cctttgcaga 960  
 tggaggagct cagtactgca gtttattcaa atgatgactt atttatttct aaggaagcac 1020

```

agataagaga aactgaaacg ttttcagatt catctccaat tgaaattata gatgagttcc 1080
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gcacagaatt gccccatgac ctttctttga agaacatata acccaaagtt gaagagaaaa 1260
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cagtattcag cattgtgagc gtaacagcct acattgcctt ggcctgctc tctgtgacca 1620
tcagctttag gatatacaag ggtgtgatec aagctatcca gaaatcagat gaaggccacc 1680
cattcagggg agttgctata tctgaggagt tggttcagaa gtacagtaat tctgctcttg 1740
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ggcatcaggc acagatagat cattatctag gacttgcaaa taagaatgtt aaagatgcta 1980
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&lt;210&gt; 42

&lt;211&gt; 642

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 42

```

Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu Ser
  1              5              10              15

```

```

Glu Leu Asn Glu Val Thr Gly Thr Lys Ile Ala Tyr Glu Thr Lys Met
      20              25              30

```

```

Asp Leu Val Gln Thr Ser Glu Val Met Gln Glu Ser Leu Tyr Pro Ala
      35              40              45

```

```

Ala Gln Leu Cys Pro Ser Phe Glu Glu Ser Glu Ala Thr Pro Ser Pro
      50              55              60

```

```

Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser Ala Val Pro
      65              70              75              80

```

```

Ser Ala Gly Ala Ser Val Ile Gln Pro Ser Ser Ser Pro Leu Glu Ala
      85              90              95

```

```

Ser Ser Val Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro Pro
      100             105             110

```

```

Pro Tyr Glu Glu Ala Met Ser Val Ser Leu Lys Lys Val Ser Gly Ile
      115             120             125

```

```

Lys Glu Glu Ile Lys Glu Pro Glu Asn Ile Asn Ala Ala Leu Gln Glu
      130             135             140

```

```

Thr Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr
      145             150             155             160

```

Lys Leu Ser Ala Glu Pro Ala Pro Asp Phe Ser Asp Tyr Ser Glu Met  
 165 170 175  
 Ala Lys Val Glu Gln Pr Val Pro Asp His Ser Glu Leu Val Glu Asp  
 180 185 190  
 Ser Ser Pr Asp Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser Ile  
 195 200 205  
 Pro Asp Val Pro Gln Lys Gln Asp Glu Thr Val Met Leu Val Lys Glu  
 210 215 220  
 Ser Leu Thr Glu Thr Ser Phe Glu Ser Met Ile Glu Tyr Glu Asn Lys  
 225 230 235 240  
 Glu Lys Leu Ser Ala Leu Pro Pro Glu Gly Gly Lys Pro Tyr Leu Glu  
 245 250 255  
 Ser Phe Lys Leu Ser Leu Asp Asn Thr Lys Asp Thr Leu Leu Pro Asp  
 260 265 270  
 Glu Val Ser Thr Leu Ser Lys Lys Glu Lys Ile Pro Leu Gln Met Glu  
 275 280 285  
 Glu Leu Ser Thr Ala Val Tyr Ser Asn Asp Asp Leu Phe Ile Ser Lys  
 290 295 300  
 Glu Ala Gln Ile Arg Glu Thr Glu Thr Phe Ser Asp Ser Ser Pro Ile  
 305 310 315 320  
 Glu Ile Ile Asp Glu Phe Pro Thr Leu Ile Ser Ser Lys Thr Asp Ser  
 325 330 335  
 Phe Ser Lys Leu Ala Arg Glu Tyr Thr Asp Leu Glu Val Ser His Lys  
 340 345 350  
 Ser Glu Ile Ala Asn Ala Pro Asp Gly Ala Gly Ser Leu Pro Cys Thr  
 355 360 365  
 Glu Leu Pro His Asp Leu Ser Leu Lys Asn Ile Gln Pro Lys Val Glu  
 370 375 380  
 Glu Lys Ile Ser Phe Ser Asp Asp Phe Ser Lys Asn Gly Ser Ala Thr  
 385 390 395 400  
 Ser Lys Val Leu Leu Leu Pro Pro Asp Val Ser Ala Leu Ala Thr Gln  
 405 410 415  
 Ala Glu Ile Glu Ser Ile Val Lys Pro Lys Val Leu Val Lys Glu Ala  
 420 425 430  
 Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp Arg Ser Pro Ser  
 435 440 445  
 Ala Ile Phe Ser Ala Glu Leu Ser Lys Thr Ser Val Val Asp Leu Leu  
 450 455 460  
 Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala Ser Leu  
 465 470 475 480

Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser Val Thr Ala  
 485 490 495  
 Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe Arg Ile Tyr  
 500 505 510  
 Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly His Pro Phe  
 515 520 525  
 Arg Glu Val Ala Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser  
 530 535 540  
 Ala Leu Gly His Val Asn Cys Thr Ile Lys Glu Leu Arg Arg Leu Phe  
 545 550 555 560  
 Leu Val Asp Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp  
 565 570 575  
 Val Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile  
 580 585 590  
 Leu Ala Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr Glu Arg His  
 595 600 605  
 Gln Ala Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Asn Val Lys  
 610 615 620  
 Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu Lys Arg Lys  
 625 630 635 640  
 Ala Glu

<210> 43  
 <211> 344  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (13)

<220>  
 <221> unsure  
 <222> (39)

<220>  
 <221> unsure  
 <222> (185)

<220>  
 <221> unsure  
 <222> (260)

<400> 43  
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 gccgtcgggc acagtcccg tgcctctctg tttctcagtc ttccgcgcgac cctcgtcggc 120  
 gccacacggg gcgggctaca agctgctcat ccagaagtcc ctcagcctgt acggcgacca 180  
 gatcnacatg caccgcaa at tcgtggcgca gctgttcgcc gaggagtggg gccagtacgt 240

ggacttgccc aagggtcttcn cggtgagcga gcgctgcaag gtgcgcctcg tgccgctgca 300  
tatccagctc actaccctgg gaaatcttac accttcaagc actg 344

<210> 44  
<211> 631  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> (73)

<220>  
<221> unsure  
<222> (369)

<400> 44  
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aaagtaaaag cantacatcc acattaacat tataacatct tacagtaata taaaagccaa 120  
atcattgttg gtacgtcatt ttctttaaag tgaacaattt aagaaaactt cacaagagtc 180  
tgcacttttg aaagatacga tcagagtaca cagtagagac aaaacaggca tcttcattgt 240  
aatttttttt aataaataaa agcacattaa caaaaaagga aggtaagcag caccggaagc 300  
ctttgacgtt tgtaactaaa tgctgggtact caattgaatc gagctggtta agtttcaacta 360  
ggaggcgcn aaaaaggagcc gtttttgact taacatttta attctagtag agataagaag 420  
agcttggttg ggcttacagt ccttcacctg actgtccttc accagttagt agcataccag 480  
ttcttcaaat gtcttatact ttggaaagca gaccgactc tggagcactc gccttaatta 540  
gattctgaat ttcttgaat tttggatggt ccttatcagc taccagctga agcagaacag 600  
cctcactcgt ggtcactatg atcccggttc g 631

<210> 45  
<211> 22  
<212> PRT  
<213> Homo sapiens

<400> 45  
Met Val Leu Ile Ser Tyr Gln Leu Lys Gln Asn Ser Leu Thr Arg Gly  
1 5 10 15

His Tyr Asp Pro Gly Ser  
20

<210> 46  
<211> 70  
<212> DNA  
<213> Homo sapiens

<400> 46  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 60  
aaaaaaaaaa 70

<210> 47  
<211> 428  
<212> DNA  
<213> Homo sapiens

<400> 47  
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tcaacatgcy ctacctgggc aagggtgctg agctggtgct gcggarcccg gcccgccacc 120  
agctggacca cgtcttttaa atcggcattg gagaactcat caccgctcg sccaagcaca 180



```

tcttcaagac gtacttacag ggagtcgagc tctccggcct ctcagccgcc atcagccact 240
tcctgaactg cttcctgagc tcctacccaa acccctgggc ccacctgccc gccgacgagc 300
tggtctccaa gaagcggaat aagaggagga aaaaccggcc cccgggggct gcagataaca 360
cagcctgggc tgtcatgacc ccccaggagc tctggaagaa catctgccag gaggccaaga 420
actacttt                                     428

```

<210> 48  
 <211> 128  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (21)

<220>  
 <221> UNSURE  
 <222> (43)

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<400> 48
Met Arg Gln Arg Gly Ile Asn Met Arg Tyr Leu Gly Lys Val Leu Glu
  1              5              10              15

Leu Val Leu Arg Xaa Pro Ala Arg His Gln Leu Asp His Val Phe Lys
      20              25              30

Ile Gly Ile Gly Glu Leu Ile Thr Arg Ser Xaa Lys His Ile Phe Lys
  35              40              45

Thr Tyr Leu Gln Gly Val Glu Leu Ser Gly Leu Ser Ala Ala Ile Ser
  50              55              60

His Phe Leu Asn Cys Phe Leu Ser Ser Tyr Pro Asn Pro Val Ala His
  65              70              75              80

Leu Pro Ala Asp Glu Leu Val Ser Lys Lys Arg Asn Lys Arg Arg Lys
      85              90              95

Asn Arg Pro Pro Gly Ala Ala Asp Asn Thr Ala Trp Ala Val Met Thr
  100              105              110

Pro Gln Glu Leu Trp Lys Asn Ile Cys Gln Glu Ala Lys Asn Tyr Phe
  115              120              125

```

<210> 49  
 <211> 245  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (46)

<220>  
 <221> unsure  
 <222> (138)

<220>  
 <221> unsure

&lt;222&gt; (147)

&lt;400&gt; 49

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 cggagagccg cttatgggtg tggtcctgcc agacaccttg tttcaagggg gatgggcgtg 120  
 agcgggcaag cagagcanc caccgntga gcaagaactt ttttttgttt ttaaaccatc 180  
 acgtcctcat ttcacattgg aataaagtga gtttttgaaa aaaaaaaaaa aaaaaaaaaa 240  
 aaaaaa 245

&lt;210&gt; 50

&lt;211&gt; 566

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 50

cagtgaagccc tttgaaaaat aaacatccag atgaagatgc tgtggaagct gaggggcatg 60  
 aggtaaaaag actcagggtt gacaaagaag gtgaagtcag agaaacagcc agtcaaacga 120  
 cttccagcga aatttcttca gttatggtag gagaaacaga agcatcatct tcatctcagg 180  
 ataaagacaa agatagccgt tgtwcccgcc agcactgtwc agaagaggat gaagaagagg 240  
 atgaagagga agaagaagag tcttttatga catcaagaga aatgatccca gaaagaaaaa 300  
 atcaagaaaa agaattctgat gatgccttaa ctgtgaatga agagacttct gagggaaaata 360  
 atcaaattgga ggaattctgat gtgtctcaag ctgagaaaga tttgctacat tctgaaggta 420  
 gtgaaaacga aggccttgta agtagtagtt cttctgactg ccgtgaaaca gaagaattag 480  
 taggatccaa ttccagtaaa actggagaga ttctttcaga atcatccatg gaaaatgatg 540  
 acgaagccac agaagtcacc gatgaa 566

&lt;210&gt; 51

&lt;211&gt; 141

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (21)

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (26)

&lt;400&gt; 51

Met Val Gly Glu Thr Glu Ala Ser Ser Ser Ser Gln Asp Lys Asp Lys  
 1 5 10 15  
 Asp Ser Arg Cys Xaa Arg Gln His Cys Xaa Glu Glu Asp Glu Glu Glu  
 20 25 30  
 Asp Glu Glu Glu Glu Glu Ser Phe Met Thr Ser Arg Glu Met Ile  
 35 40 45  
 Pro Glu Arg Lys Asn Gln Glu Lys Glu Ser Asp Asp Ala Leu Thr Val  
 50 55 60  
 Asn Glu Glu Thr Ser Glu Glu Asn Asn Gln Met Glu Glu Ser Asp Val  
 65 70 75 80  
 Ser Gln Ala Glu Lys Asp Leu Leu His Ser Glu Gly Ser Glu Asn Glu  
 85 90 95  
 Gly Pro Val Ser Ser Ser Ser Ser Asp Cys Arg Glu Thr Glu Glu Leu  
 100 105 110

Val Gly Ser Asn Ser Ser Lys Thr Gly Glu Ile Leu Ser Glu Ser Ser  
 115 120 125

Met Glu Asn Asp Asp Glu Ala Thr Glu Val Thr Asp Glu  
 130 135 140

<210> 52  
 <211> 531  
 <212> DNA  
 <213> Homo sapiens

<400> 52  
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 tactgactga cttgactgtc aggttcacaa cagctagatg atatatattat gactatgtct 120  
 aatagttgaa ataaaatctg aatattgatt tactataccc aagaggggag aaaaattaac 180  
 cattgtaaat ttttaaaaaat tttttcaaaa atgttaaaat gaggcaaatt taagtttaca 240  
 aattttgaaa ttttcttttg aatatttatg aaattgtcag taaacttacc taagatcctg 300  
 tgaccttttg atatttttta ttttaattgt agtgccatgg accatttgta aacaaattga 360  
 tttacttttg ttggttgtaa gttgaagatt tagcattatg actttgaggt ctgtgggtttt 420  
 atttgtaaac ttgcaattgc tatatttgca agggcaaatg tatttcttta ttaaataaaag 480  
 tacaataatg gtgaatgtac caaaatgaca tcacttaaaa aaaaaaaaaa a 531

<210> 53  
 <211> 1163  
 <212> DNA  
 <213> Homo sapiens

<400> 53  
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 gctaacaagc ccctgggacc gaggggcagc agcakgtgca tggcgagaag aaggagctcc 180  
 agcagtcccc tcagccccac cctcctatga ggaaccacct ctggggaggg gatgaaggca 240  
 ggggccttcc cccagcccc cacagcgggt cctctccacc ctactgtggc ctatgtggac 300  
 cccagcagca gctccagcta tgacaacggt ttccccaccg gagacatga gctcttcacc 360  
 actttcagct gggatgacca gaaagtctgt cgagtctttg tcagaaaggc ctacaccatc 420  
 ctgctgatcc agctgctggt gaccttggct gtctgtggct tctttacttt ctgtgacctt 480  
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 gcaacctacc tgacctggc ttgctgttct ggaccagga ggcatttccc ctggaacctg 600  
 atttctctga cgtctttac cctgtccatg gcctacctca ctgggatgct gtccagctac 660  
 tacaacacca cctcgtgct gctgtgcctg ggcacacgg ccctgtctg cctctcagtc 720  
 accgtcttca gcttccagac caagttcgac ttcacctcct gccagggcgt gctcttcgtg 780  
 cttctcatga ctcttttctt cagcggactc atcctggcca tcctcctacc cttccaatat 840  
 gtgccctggc tccatgcagt ttatgcagca ctgggagcgg gtgtatttac attgttcctg 900  
 gcacttgaca cccagttgct gatgggtaac cgacgccact cgctgagccc tgaggagtat 960  
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 gccaacccaa aaaaaaaaaa aaa 1163

<210> 54  
 <211> 270  
 <212> PRT  
 <213> Homo sapiens

<400> 54  
 Met Lys Ala Gly Ala Phe Pro Pro Ala Pro Thr Ala Val Pro Leu His  
 1 5 10 15

Pro Ser Trp Ala Tyr Val Asp Pro Ser Ser Ser Ser Ser Tyr Asp Asn  
                   20                  25                  30  
 Gly Phe Pro Thr Gly Asp His Glu Leu Phe Thr Thr Phe Ser Trp Asp  
                   35                  40                  45  
 Asp Gln Lys Val Arg Arg Val Phe Val Arg Lys Val Tyr Thr Ile Leu  
                   50                  55                  60  
 Leu Ile Gln Leu Leu Val Thr Leu Ala Val Val Ala Leu Phe Thr Phe  
                   65                  70                  75                  80  
 Cys Asp Pro Val Lys Asp Tyr Val Gln Ala Asn Pro Gly Trp Tyr Trp  
                   85                  90                  95  
 Ala Ser Tyr Ala Val Phe Phe Ala Thr Tyr Leu Thr Leu Ala Cys Cys  
                   100                  105                  110  
 Ser Gly Pro Arg Arg His Phe Pro Trp Asn Leu Ile Leu Leu Thr Val  
                   115                  120                  125  
 Phe Thr Leu Ser Met Ala Tyr Leu Thr Gly Met Leu Ser Ser Tyr Tyr  
                   130                  135                  140  
 Asn Thr Thr Ser Val Leu Leu Cys Leu Gly Ile Thr Ala Leu Val Cys  
                   145                  150                  155                  160  
 Leu Ser Val Thr Val Phe Ser Phe Gln Thr Lys Phe Asp Phe Thr Ser  
                   165                  170                  175  
 Cys Gln Gly Val Leu Phe Val Leu Leu Met Thr Leu Phe Phe Ser Gly  
                   180                  185                  190  
 Leu Ile Leu Ala Ile Leu Leu Pro Phe Gln Tyr Val Pro Trp Leu His  
                   195                  200                  205  
 Ala Val Tyr Ala Ala Leu Gly Ala Gly Val Phe Thr Leu Phe Leu Ala  
                   210                  215                  220  
 Leu Asp Thr Gln Leu Leu Met Gly Asn Arg Arg His Ser Leu Ser Pro  
                   225                  230                  235                  240  
 Glu Glu Tyr Ile Phe Gly Ala Leu Asn Ile Tyr Leu Asp Ile Ile Tyr  
                   245                  250                  255  
 Ile Phe Thr Phe Phe Leu Gln Leu Phe Gly Thr Asn Arg Glu  
                   260                  265                  270

&lt;210&gt; 55

&lt;211&gt; 624

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (123)

&lt;400&gt; 55

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cggcgggcgg ggcgggcggt ggcactggct ccggactctg cccggccagg gcggcggmte 120  
 canccgggag ggcgacgtgg agcgccack tggakcgcc cgggggargc tggcggcggg 180  
 akgcgagggc cgggcggcgc akcakccakg agcgcccacg gagstggacc ccagakccg 240  
 cgcggcgcgc cagcagttcc aggaaggatg ttaccttga cgatgacagt gttaatcctg 300  
 ctgctgctcc ccacgggtca ggctgcccc aaggatggag tcacaaggcc agaactctgaa 360  
 gtgcagcatc agctcctgcc caacccttc cagccaggcc aggagcagct cggacttctg 420  
 cagagctacc taaagggact aggaaggaca gaagtgaac tggagcatct gagccgggag 480  
 caggttctcc tctacctctt tgccctccat gactatgacc agagtggaca gctggatggc 540  
 ctggagctgc tgtccatggt gacagctgct ctggcccctg gagctgcca ctctcctacc 600  
 accaaccgg tgatcttgat agtg 624

<210> 56

<211> 119

<212> PRT

<213> Homo sapiens

<400> 56

Met Leu Pro Leu Thr Met Thr Val Leu Ile Leu Leu Leu Leu Pro Thr  
 1 5 10 15

Gly Gln Ala Ala Pro Lys Asp Gly Val Thr Arg Pro Glu Ser Glu Val  
 20 25 30

Gln His Gln Leu Leu Pro Asn Pro Phe Gln Pro Gly Gln Glu Gln Leu  
 35 40 45

Gly Leu Leu Gln Ser Tyr Leu Lys Gly Leu Gly Arg Thr Glu Val Gln  
 50 55 60

Leu Glu His Leu Ser Arg Glu Gln Val Leu Leu Tyr Leu Phe Ala Leu  
 65 70 75 80

His Asp Tyr Asp Gln Ser Gly Gln Leu Asp Gly Leu Glu Leu Leu Ser  
 85 90 95

Met Leu Thr Ala Ala Leu Ala Pro Gly Ala Ala Asn Ser Pro Thr Thr  
 100 105 110

Asn Pro Val Ile Leu Ile Val  
 115

<210> 57

<211> 80

<212> DNA

<213> Homo sapiens

<400> 57

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 aaaaaaaaaa aaaaaaaaaa 80

<210> 58

<211> 2160

<212> DNA

<213> Homo sapiens

<400> 58

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 caaattaact gatcagacca caacttttca atgttttaaa cagaataagc ttcctgtaa 180

```

aagcagcacc tttgtgacgt ttttaacttta gtatttctct ccttcttctt caccctctcc 240
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attcttactg caagcgggag gcgaggagc ggaagcggc ggagcgcgag gcgcgcgaga 360
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```

&lt;210&gt; 59

&lt;211&gt; 141

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 59

```

Met Asn His Arg Tyr Ser Tyr Cys Lys Arg Glu Ala Glu Glu Arg Glu
 1             5             10             15

Ala Ala Glu Arg Glu Ala Arg Glu Lys Gly His Leu Glu Pro Thr Glu
 20             25             30

Leu Leu Met Asn Arg Ala Tyr Leu Gln Ser Ile Thr Pro Gln Gly Tyr
 35             40             45

Ser Asp Ser Glu Glu Arg Glu Ser Met Pro Arg Asp Gly Glu Ser Glu
 50             55             60

Lys Glu His Glu Lys Glu Gly Glu Asp Gly Tyr Gly Lys Leu Gly Arg
 65             70             75             80

Gln Asp Gly Asp Glu Glu Phe Glu Glu Glu Glu Glu Ser Glu Asn
 85             90             95

Lys Ser Met Asp Thr Asp Pro Glu Thr Ile Arg Asp Glu Glu Glu Thr
100            105            110

```

Gly Asp His Ser Met Asp Asp Ser Ser Glu Asp Gly Lys Met Glu Thr  
 115 120 125

Lys Ser Asp His Glu Glu Asp Asn Met Glu Asp Gly Met  
 130 135 140

<210> 60

<211> 2168

<212> DNA

<213> Homo sapiens

<400> 60

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agtatgagac gaacaaagtc actcggatcc agagcatgaa ttatggcacc attaatgtgg 180
tcttccacgt gatcatcttt tcttacgttt gctttgtctc ggtgagtgac aagctgtacc 240
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```

<210> 61

<211> 595

<212> PRT

<213> Homo sapiens

<400> 61

Met Pro Ala Cys Cys Ser Cys Ser Asp Val Phe Gln Tyr Glu Thr Asn  
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Lys Val Thr Arg Ile Gln Ser Met Asn Tyr Gly Thr Ile Lys Trp Phe  
 20 25 30  
 Phe His Val Ile Ile Phe Ser Tyr Val Cys Phe Ala Leu Val Ser Asp  
 35 40 45  
 Lys Leu Tyr Gln Arg Lys Glu Pro Val Ile Ser Ser Val His Thr Lys  
 50 55 60  
 Val Lys Gly Ile Ala Glu Val Lys Glu Glu Ile Val Glu Asn Gly Val  
 65 70 75 80  
 Lys Lys Leu Val His Ser Val Phe Asp Thr Ala Asp Tyr Thr Phe Pro  
 85 90 95  
 Leu Gln Gly Asn Ser Phe Phe Val Met Thr Asn Phe Leu Lys Thr Glu  
 100 105 110  
 Gly Gln Glu Gln Arg Leu Cys Pro Glu Tyr Pro Thr Arg Arg Thr Leu  
 115 120 125  
 Cys Ser Ser Asp Arg Gly Cys Lys Lys Gly Trp Met Asp Pro Gln Ser  
 130 135 140  
 Lys Gly Ile Gln Thr Gly Arg Cys Val Val His Glu Gly Asn Gln Lys  
 145 150 155 160  
 Thr Cys Glu Val Ser Ala Trp Cys Pro Ile Glu Ala Val Glu Glu Ala  
 165 170 175  
 Pro Arg Pro Ala Leu Leu Asn Ser Ala Glu Asn Phe Thr Val Leu Ile  
 180 185 190  
 Lys Asn Asn Ile Asp Phe Pro Gly His Asn Tyr Thr Thr Arg Asn Ile  
 195 200 205  
 Leu Pro Gly Leu Asn Ile Thr Cys Thr Phe His Lys Thr Gln Asn Pro  
 210 215 220  
 Gln Cys Pro Ile Phe Arg Leu Gly Asp Ile Phe Arg Glu Thr Gly Asp  
 225 230 235 240  
 Asn Phe Ser Asp Val Ala Ile Gln Gly Gly Ile Met Gly Ile Glu Ile  
 245 250 255  
 Tyr Trp Asp Cys Asn Leu Asp Arg Trp Phe His His Cys His Pro Lys  
 260 265 270  
 Tyr Ser Phe Arg Arg Leu Asp Asp Lys Thr Thr Asn Val Ser Leu Tyr  
 275 280 285  
 Pro Gly Tyr Asn Phe Arg Tyr Ala Lys Tyr Tyr Lys Glu Asn Asn Val  
 290 295 300  
 Glu Lys Arg Thr Leu Ile Lys Val Phe Gly Ile Arg Phe Asp Ile Leu  
 305 310 315 320  
 Val Phe Gly Thr Gly Gly Lys Phe Asp Ile Ile Gln Leu Val Val Tyr  
 325 330 335



Ile Gly Ser Thr Leu Ser Tyr Phe Gly Leu Ala Ala Val Phe Ile Asp  
                   340                  345                  350  
 Phe Leu Ile Asp Thr Tyr Ser Ser Asn Cys Cys Arg Ser His Ile Tyr  
                   355                  360                  365  
 Pro Trp Cys Lys Cys Cys Gln Pro Cys Val Val Asn Glu Tyr Tyr Tyr  
                   370                  375                  380  
 Arg Lys Lys Cys Glu Ser Ile Val Glu Pro Lys Pro Thr Leu Lys Tyr  
                   385                  390                  395                  400  
 Val Ser Phe Val Asp Glu Ser His Ile Arg Met Val Asn Gln Gln Leu  
                   405                  410                  415  
 Leu Gly Arg Ser Leu Gln Asp Val Lys Gly Gln Glu Val Pro Arg Pro  
                   420                  425                  430  
 Ala Met Asp Phe Thr Asp Leu Ser Arg Leu Pro Leu Ala Leu His Asp  
                   435                  440                  445  
 Thr Pro Pro Ile Pro Gly Gln Pro Glu Glu Ile Gln Leu Leu Arg Lys  
                   450                  455                  460  
 Glu Ala Thr Pro Arg Ser Arg Asp Ser Pro Val Trp Cys Gln Cys Gly  
                   465                  470                  475                  480  
 Ser Cys Leu Pro Ser Gln Leu Pro Glu Ser His Arg Cys Leu Glu Glu  
                   485                  490                  495  
 Leu Cys Cys Arg Lys Lys Pro Gly Ala Cys Ile Thr Thr Ser Glu Leu  
                   500                  505                  510  
 Phe Arg Lys Leu Val Leu Ser Arg His Val Leu Gln Phe Leu Leu Leu  
                   515                  520                  525  
 Tyr Gln Glu Pro Leu Leu Ala Leu Asp Val Asp Ser Thr Asn Ser Arg  
                   530                  535                  540  
 Leu Arg His Cys Ala Tyr Arg Cys Tyr Ala Thr Trp Arg Phe Gly Ser  
                   545                  550                  555                  560  
 Gln Asp Met Ala Asp Phe Ala Ile Leu Pro Ser Cys Cys Arg Trp Arg  
                   565                  570                  575  
 Ile Arg Lys Glu Phe Pro Lys Ser Glu Gly Gln Tyr Ser Gly Phe Lys  
                   580                  585                  590  
 Ser Pro Tyr  
                   595

&lt;210&gt; 62

&lt;211&gt; 430

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 62

taaagatctg tgttcagagt cataactgaay agagacttct ggactctata gaaccactg 60

```

cctcctgatg aagtccttac tggtcaccct tgcagttttt atgctcctgg cccaattggg 120
ctcaggtaat tggatgtga aaaagtgtct aaacgacgtt ggaatttgca agaagaagtg 180
caaacctgaa gagatgcatg taaagaatgg ttgggcaatg tgcggcaaac aaagggactg 240
ctgtgttcca gctgacagac gtgctaatta tcctgttttc tgtgtccaga caaagactac 300
aagaatttca acagtaacag caacaacagc aacaacaact ttgatgatga ctactgcttc 360
gatgtcttcg atggctccta cccgtttctc ccactgggtg aacattccag cctctgtctc 420
ctgctctagg                                     430

```

&lt;210&gt; 63

&lt;211&gt; 121

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 63

```

Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln
  1             5             10            15
Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly
             20             25            30
Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly
             35             40            45
Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg
             50             55            60
Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile
             65             70            75            80
Ser Thr Val Thr Ala Thr Thr Ala Thr Thr Thr Leu Met Met Thr Thr
             85             90            95
Ala Ser Met Ser Ser Met Ala Pro Thr Arg Phe Ser His Trp Leu Asn
            100            105            110
Ile Pro Ala Ser Val Ser Cys Ser Arg
            115            120

```

&lt;210&gt; 64

&lt;211&gt; 112

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (8)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (12)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (36)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (41)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (44)

&lt;400&gt; 64

tttcctgntt tnggatcccc gattcattaa agcaangggg nttnaaaaaa aaaaaaaaaa 60  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 112

&lt;210&gt; 65

&lt;211&gt; 324

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (1)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (69)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (74)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (125)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (159)

&lt;400&gt; 65

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 ggggtgtacnc gtanggggtct gtgtgctggg ggtggctcac cgggcagcgt gggtgagcgg 120  
 cgcancggcg gcagcggaga acgagagagg ggagcagana cagaatcgcc taagctgaag 180  
 tgtattggcg ccatcatggc tcaactgcggc ctccggctcc ttggctcggg tgattctcct 240  
 gcctgagcct ccctagtagc taggactaca gtgctgtaga agaaaatcac atgattgggtg 300  
 ccctcaaaaa attggtgccca cttg 324

&lt;210&gt; 66

&lt;211&gt; 794

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (61)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (82)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (108)..(120)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (184)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (754)

&lt;400&gt; 66

```

cattattttca tcaccagaga atacacatgc agcaaatagc attgtgagtc aaactattcc 60
naaagcacag attcagcaat cnacacacac tcattctggat atctcacnnn nnnnnnnnnn 120
ttaactgatg aaaaaagtaa tggaacaatt gcccttctgg atgattctga ggatcctgga 180
gccnatgtat ctaacataca gcttcagcaa aaaatttcaa gtctggagat taaactcaaa 240
gtatctgaag aagaaaaaca gagaattaaa caggatgtgg aakcattgat ggaaaagcat 300
aatgtcttag aaaaaggctt tctaaaagaa aaagagcaag aggccatttc ttttcaagat 360
agatacaaaag aacttcagga aaaacataaa caagaattgg aagacatgag gaaagctggg 420
cacgaagccc tcagcattat tgtggatgaa tataaggcac tactgcagtc ttcagttaag 480
caacaagtag aagctattga aaaacagtac atttctgcaa ttgagaaaca ggcacacaag 540
tgtgaggagt tgctaaatgc tcagcatcag aggctccttg aagtgcctaga tacagagaag 600
gaactgttaa aagaaaaaat aaaggaagct ttgattcagc aatctcaaga acagaaggaa 660
atattggaaa agtgtttgga ggaagaaagg caaagaaata aagaggcatt agtatccgct 720
gcaaagcttg aaaaagaacc agtgaaggat gcanttttaa aattcgtaga agaagaaaga 780
aaaaaaaaaa aaaa

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794

&lt;210&gt; 67

&lt;211&gt; 164

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (156)

&lt;400&gt; 67

```

Met Glu Lys His Asn Val Leu Glu Lys Gly Phe Leu Lys Glu Lys Glu
 1             5             10             15

Gln Glu Ala Ile Ser Phe Gln Asp Arg Tyr Lys Glu Leu Gln Glu Lys
 20             25             30

His Lys Gln Glu Leu Glu Asp Met Arg Lys Ala Gly His Glu Ala Leu
 35             40             45

Ser Ile Ile Val Asp Glu Tyr Lys Ala Leu Leu Gln Ser Ser Val Lys
 50             55             60

Gln Gln Val Glu Ala Ile Glu Lys Gln Tyr Ile Ser Ala Ile Glu Lys
 65             70             75             80

Gln Ala His Lys Cys Glu Glu Leu Leu Asn Ala Gln His Gln Arg Leu
 85             90             95

Leu Glu Val Leu Asp Thr Glu Lys Glu Leu Leu Lys Glu Lys Ile Lys
100            105            110

Glu Ala Leu Ile Gln Gln Ser Gln Glu Gln Lys Glu Ile Leu Glu Lys
115            120            125

Cys Leu Glu Glu Glu Arg Gln Arg Asn Lys Glu Ala Leu Val Ser Ala
130            135            140

Ala Lys Leu Glu Lys Glu Pro Val Lys Asp Ala Xaa Leu Lys Phe Val

```

145

150

155

160

Glu Glu Glu Arg

&lt;210&gt; 68

&lt;211&gt; 1494

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 68

```

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cctgtgttcc cgggtcatgt tgagtaggaa taaataaatc tgatgctgcc tcttgaaaaa 1440
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1494

```

&lt;210&gt; 69

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 69

```

Met Ser Ala Gln Ala Gln Met Arg Ala Leu Leu Asp Gln Leu Met Gly
  1              5              10              15

Thr Ala Arg Asp Gly Asp Glu Thr Arg Gln Arg Val Lys Phe Thr Asp
  20              25              30

Asp Arg Val Cys Lys Ser His Leu Leu Asp Cys Cys Pro His Asp Ile
  35              40              45

Leu Ala Gly Thr Arg Met Asp Leu Gly Glu Cys Thr Lys Ile His Asp
  50              55              60

Leu Ala Leu Arg Ala Asp Tyr Glu Ile Ala Ser Lys Glu Arg Asp Leu
  65              70              75              80

Phe Phe Glu Leu Asp Ala Met Asp His Leu Glu Ser Phe Ile Ala Glu

```

caagggaaagt	tctgagggct	gagaggttgc	tcattctgtca	gagcgtgctg	cccaccctcc	60
acccttgcac	ggcagaaact	gtgcagggga	cgaggccaag	gaatcaggag	accagagagc	120
aggggtggcc	cggagacggt	gaagaaacca	agacgcagag	aggccaagcc	ccttgccttg	180
ggtcacacac	ctaaagcagag	cagagccaga	actcacaaac	agatccagac	gcaacaggga	240
catggccacc	cggagcgaag	aggcagtcac	ccgcagggcc	aaggtggctc	ccgtgagag	300
catgaqcaag	ttcttaaggc	acttcacggt	cgtgggagac	gactaccatg	cctggaacat	360

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caactacaag aaatgggaga atgaagagga ggaggaggag gaggagcagc caccacccac 420
accagtctca ggcgaggaag gcagagctgc agccccctgac gttgccccctg cccctggccc 480
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gtttcagggtc atcatcatct gcttggtggt tctggatgcc ctcttggtgc ttgctgagct 600
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aaaaaaaaaa aaaaaaaaaa a 1761

```

&lt;210&gt; 71

&lt;211&gt; 273

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 71

```

Met Ala Thr Trp Asp Glu Lys Ala Val Thr Arg Arg Ala Lys Val Ala
  1                      5                      10                      15

Pro Ala Glu Arg Met Ser Lys Phe Leu Arg His Phe Thr Val Val Gly
          20                      25                      30

Asp Asp Tyr His Ala Trp Asn Ile Asn Tyr Lys Lys Trp Glu Asn Glu
          35                      40                      45

Glu Glu Glu Glu Glu Glu Gln Pro Pro Pro Thr Pro Val Ser Gly
          50                      55                      60

Glu Glu Gly Arg Ala Ala Ala Pro Asp Val Ala Pro Ala Pro Gly Pro
          65                      70                      75                      80

Ala Pro Arg Ala Pro Leu Asp Phe Arg Gly Met Leu Arg Lys Leu Phe
          85                      90                      95

Ser Ser His Arg Phe Gln Val Ile Ile Ile Cys Leu Val Val Leu Asp
          100                      105                      110

Ala Leu Leu Val Leu Ala Glu Leu Ile Leu Asp Leu Lys Ile Ile Gln
          115                      120                      125

Pro Asp Lys Asn Asn Tyr Ala Ala Met Val Phe His Tyr Met Ser Ile
          130                      135                      140

Thr Ile Leu Val Phe Phe Met Met Glu Ile Ile Phe Lys Leu Phe Val
          145                      150                      155                      160

```

Phe Arg Leu Glu Phe Phe His His Lys Phe Glu Ile Leu Asp Ala Val  
 165 170 175  
 Val Val Val Val Ser Phe Ile Leu Asp Ile Val Leu Leu Phe Gln Glu  
 180 185 190  
 His Gln Phe Glu Ala Leu Gly Leu Leu Ile Leu Leu Arg Leu Trp Arg  
 195 200 205  
 Val Ala Arg Ile Ile Asn Gly Ile Ile Ile Ser Val Lys Thr Arg Ser  
 210 215 220  
 Glu Arg Gln Leu Leu Arg Leu Lys Gln Met Asn Val Gln Leu Ala Ala  
 225 230 235 240  
 Lys Ile Gln His Leu Glu Phe Ser Cys Ser Glu Lys Glu Gln Glu Ile  
 245 250 255  
 Glu Arg Leu Asn Lys Leu Leu Arg Gln His Gly Leu Leu Gly Glu Val  
 260 265 270

Asn

<210> 72  
 <211> 928  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (367)

<220>  
 <221> unsure  
 <222> (448)

<220>  
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 <222> (467)

<220>  
 <221> unsure  
 <222> (508)

<220>  
 <221> unsure  
 <222> (539)

<400> 72  
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 catgaataca acctaacgca tctgcagcct tccacagatt atgaagtgtg tctcacagt 180  
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 aaaaaantac caccactcat taaaaaagta tatgcaaaaa acctcttcaa tcccactaaa 420  
 tgagctgtac ccaccactca ttaacctntg ggaaggtgac agcgagnaag acaaagatgg 480



```

ttttgcagac accaagccaa cccaggtnga cacatccaga aggtattaca tgtggtaant 540
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agtgtcfaat aaaatgatta atgacaggat ggggttcccc tgtgctttta ccagtagcat 900
gacccttcct gaagccatcc gtagaaag 928

```

&lt;210&gt; 73

&lt;211&gt; 52

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

```

Met Ile Val Ile Ile Leu Leu Phe Tyr Phe Ser Cys Cys Ala Lys Leu
1             5             10             15

```

```

Asn Asn Ala Val Leu Thr Thr Val Leu Asn Lys Met Ile Asn Asp Arg
20             25             30

```

```

Met Gly Phe Pro Cys Ala Phe Thr Ser Ser Met Thr Leu Pro Glu Ala
35             40             45

```

```

Ile Arg Arg Lys
50

```

&lt;210&gt; 74

&lt;211&gt; 49

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (9)

&lt;400&gt; 74

```

aaattaaana aaaaaaaaaa aaaaaaaaaa aaataaagaa aaaaaaaaaa 49

```

&lt;210&gt; 75

&lt;211&gt; 597

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 75

```

attctacaag ataacttccc agtactttaa aaaagtctca aagtcataaa caagaaagaa 60
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attaaatcct ggaccagcaa aaggacatta gtgggaaaac tgatgaaatt caaatgagat 180
cttataattga agttaattgt gtcagtgtac atttcctggc tttcataatt gcaagtgtat 240
atgtaagggtt tgtaaatatt aggagcagct gggtaaaggc tatacaaaaa ctctatacta 300
tttttgcatt tttttctgta agttttaaac attttccaac taaaaagttg aaaacacatg 360
tattagagac acatgcgtat gtgtctctaa taatcttaaa tatatttaag atgatagaag 420
gaattcttga gatagtaaaa tgaagtcacc aaaaaacaaa caaagaaaca aaacgaaatc 480
accaaaatct atcaataaat ttcaggtaat acttttggca gattcattcc tttgagatgg 540
agtctcactc ccagtctggg caacgagcga aactccgtct aaaaaaaaaa aaaaaaa 597

```

&lt;210&gt; 76

&lt;211&gt; 89

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 76

Met Arg Ser Tyr Ile Glu Val Asn Cys Val Ser Val His Phe Leu Val  
 1 5 10 15

Phe Ile Ile Ala Ser Asp Tyr Val Arg Phe Val Asn Ile Arg Ser Ser  
 20 25 30

Trp Val Lys Val Ile Gln Lys Leu Tyr Thr Ile Phe Ala Phe Phe Ser  
 35 40 45

Val Ser Leu Lys His Phe Pro Thr Lys Lys Leu Lys Thr His Val Leu  
 50 55 60

Glu Thr His Ala Tyr Val Ser Leu Ile Ile Leu Asn Ile Phe Lys Met  
 65 70 75 80

Ile Glu Gly Ile Leu Glu Ile Val Lys  
 85

&lt;210&gt; 77

&lt;211&gt; 1804

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (1794)

&lt;400&gt; 77

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 gtcactttca gatttcaatt tgaggttaag tatataaagc acatcccaat tttatatgct 180  
 gccttgagaa aattacagga tgacaggcaa tttgtaggaa tttcaaattg gatcatttaa 240  
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 ctatgtgtgc ttgttaacag ggggtggaatg tataaccatc agattcagca tgtgatttca 360  
 cctttgaatc tgagtatttc ttccctatct tctttgagtc atttttgag cagactgtca 420  
 ccagtattga taactaagca ttaaaggga aagttgcatt gcaactatgc attggtttcc 480  
 tggaagaact tttcttttgc tttagtgaat gaagaggctt gatgggatca cttactgtaa 540  
 ctcttctac ataaggaccc ctcttgcaag cagaacacaa aagaacatgc tcaaggagta 600  
 tcccattttc tggataaatt gaagaagttt gctagtaatg tctttatact agcgtcttcc 660  
 ttgtatccct ttgctggcaa gggaatacaa ggcgtcaaga ccacagatca aaacacccca 720  
 catttgagtg gagtcttatt tttactccaa gagcagttat tcccttctag tctaaaattg 780  
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 tcgagaatta ggcctcactt tataacccaa ggcattggaag tgcatgcatt ctcttagctg 960  
 ggcaaacaat tatactgtag ttgtgataca acacatgttg cttttatttg tactgcacat 1020  
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agagcatcat gattttcagt gtttgagaga aaattgatgg aaaaagtttg cagtacttga 1740  
 catgtatttg catgcacaaa ataaaattat ttgtccacct taaaaaaaaa aaanaaaaaa 1800  
 aaaa 1804

<210> 78  
 <211> 37  
 <212> PRT  
 <213> Homo sapiens

<400> 78  
 Met Lys Arg Leu Asp Gly Ile Thr Tyr Cys Asn Ser Phe Tyr Ile Arg  
 1 5 10 15

Thr Pro Ser Ala Ser Arg Thr Gln Lys Asn Met Leu Lys Glu Tyr Pro  
 20 25 30

Ile Phe Trp Ile Asn  
 35

<210> 79  
 <211> 360  
 <212> DNA  
 <213> Homo sapiens

<400> 79  
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 gcacataatt cactggattg aaagcaaagc ctcatttggg gatgaatgta gccaccacgc 180  
 ctacctgcat gaccagttct ggagctactg gaatagggtc ccaatataac agacaaatgg 240  
 tgaacacagag ggatactcac taggaaacag atttgggcca ggcttagtca tctattggtg 300  
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<210> 80  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<400> 80  
 Met Asp Leu Ser Arg Ser Trp Thr Ala Thr Gly Lys Gly Ala Ser Cys  
 1 5 10 15

Ser Lys Pro Val  
 20

<210> 81  
 <211> 202  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (136)

<220>  
 <221> unsure  
 <222> (138)

<400> 81

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aaaaaaaaa aaaaantnaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 180
aaaaaaaaa aaaaaaaaaa aa                                     202

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<210> 82  
 <211> 1189  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (1155)

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<400> 82
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agagagaata ratggtaaat gtttcttttc aggtctttta aagtgtcagg ctatcagtta 180
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ctccacagat gcaaattttc tctacaaaag atggccttgc agagccacct cagtctgttg 300
tccctgtagc agccatttca aattatgtca aagagatata ttttggggta aaatattttg 360
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ttgaattttc atttcaaaat gttttcctag tttttttct cttttttgtt ttattgtaag 480
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cagtatggta tgattaaatc aagtatttaa cctatccttc acgttaaag cttaaatttt 600
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gtgcaacaga actcnaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1189

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<210> 83  
 <211> 56  
 <212> PRT  
 <213> Homo sapiens

```

<400> 83
Met Arg Thr Phe Glu Ile Tyr Ser Trp Lys Val Lys Lys Asn Leu Arg
  1             5             10             15

Thr Pro Gln Ile Lys Ala Met Lys Leu Asn Cys Ala Thr Ser Ser Ser
          20             25             30

Lys Trp Lys Leu Val Phe Gln Val Gln Asn Lys Asn Lys Thr His Phe
          35             40             45

Phe Thr Cys Leu Lys Met Cys Thr
          50             55

```

<210> 84  
 <211> 525  
 <212> DNA  
 <213> Homo sapiens

<400> 84  
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gaaaaaagaa gtatcagtga cagcgatgaa tttagcttcag ggttttttgt gttcccttac 180  
ccatatccat ttgcccact tccaccaatt ccatttccaa gatttccatg gtttagacgt 240  
aattttccta ttccaatacc tgaatctgcc cctacaactc cccttcctag cgaaaagtaa 300  
acaagaagga aaagtcacga taaacctggt cacctgaaat tgaaattgag ccacttcctt 360  
gaagaatcaa aattcctgtt aataaaagaa aaacaaatgt aattgaaata gcacacagca 420  
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aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 525

<210> 85  
<211> 85  
<212> PRT  
<213> Homo sapiens

<400> 85  
Met Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val  
1 5 10 15  
Gly Phe Pro Val Ser Gln Asp Gln Glu Arg Glu Lys Arg Ser Ile Ser  
20 25 30  
Asp Ser Asp Glu Leu Ala Ser Gly Phe Phe Val Phe Pro Tyr Pro Tyr  
35 40 45  
Pro Phe Arg Pro Leu Pro Pro Ile Pro Phe Pro Arg Phe Pro Trp Phe  
50 55 60  
Arg Arg Asn Phe Pro Ile Pro Ile Pro Glu Ser Ala Pro Thr Thr Pro  
65 70 75 80  
Leu Pro Ser Glu Lys  
85

<210> 86  
<211> 349  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> (9)

<220>  
<221> unsure  
<222> (159)

<220>  
<221> unsure  
<222> (188)

<220>  
<221> unsure  
<222> (230)

<220>  
<221> unsure  
<222> (232)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (270)

&lt;400&gt; 86

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 ggaggggtcct cgccccggc ctgcctacct gaaaaccana actgatggct ctatttgcag 180  
 tctttcanac aacattcttc ttaacattgc tgtccttgag gacttaccan antgaagtct 240  
 tggctgaacg ttaccattg actcctgtn tcacttaaag tttccaccaa ttctacgcgt 300  
 cagagtttgc acttacaatg gactgtccac aaccttcctt atcatcagg 349

&lt;210&gt; 87

&lt;211&gt; 563

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (63)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (83)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (116)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (177)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (183)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (228)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (240)

&lt;400&gt; 87

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 acccaggatg tgcctcgggtg atttccagtg gaagaatgta ggtcccaata ccacaagcac 300  
 agtcattagc acagatgctt ttaggccagg agttcgatat gacttcagaa tttatgggtt 360  
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 ctcttccaga caaccctcac gtgctggttg atacattgac atccactcc ttcactctga 480  
 gttggaaaga ttactctact gaatctcaac ctgggtttat acaaggggtac catgtctatc 540  
 tgaaatccaa ggcgaggcag tgc 563

&lt;210&gt; 88

&lt;211&gt; 58

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 88

Arg Lys Lys Thr Gly Tyr Ser Gln Glu Leu Ala Pro Ser Asp Asn Pro  
 1 5 10 15

His Val Leu Val Asp Thr Leu Thr Ser His Ser Phe Thr Leu Ser Trp  
 20 25 30

Lys Asp Tyr Ser Thr Glu Ser Gln Pro Gly Phe Ile Gln Gly Tyr His  
 35 40 45

Val Tyr Leu Lys Ser Lys Ala Arg Gln Cys  
 50 55

&lt;210&gt; 89

&lt;211&gt; 361

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (102)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (105)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (153)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (186)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (191)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (252)..(253)

&lt;400&gt; 89

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 ccattcacta gtgctggtga aggccccagt gcnacgttca cgaagggtcac gactccggat 180  
 gaacantcct ngatgctgat tcatatccta ctgcccattgg ttttctgcgt cttgctcatc 240  
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&lt;210&gt; 90

&lt;211&gt; 756

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<220>  
 <221> unsure  
 <222> (37)

<220>  
 <221> unsure  
 <222> (54)

<220>  
 <221> unsure  
 <222> (376)

<220>  
 <221> unsure  
 <222> (433)

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 tgccaatgga aagatcctgt tctataatgt agttgtagaa aacctagaca aaccatccag 180  
 ttcagagctc cattccattc cagcaccagc caacagcaca aaactaatcc ttgacagggtg 240  
 ttccctacaa atctgctgca tagccaacaa cagtgtgggt gcttctcctg cttctgtaat 300  
 agtcatytct gcagaccccg aaaacaaaga gggtgaggaa gaaagaattg caggcacaga 360  
 ggggtgattt ttttntttt ggaaaccca acctggagat gttatagggt atgttggtgga 420  
 ctggtgtgac canaccagg atgtgectcg gtgatttcca gtggaagaat gtaggtccca 480  
 ataccacaag cacagtcatt agcacagatg cttttaggcc aggagtcca tatgacttca 540  
 gaatttatgg gttatctaca aaaaggattg cttgtttatt agagaaaaaa aacaggatac 600  
 tctcaggaac ttgtccttc agacaaccct cacgtgctgg tggatacatt gacatccac 660  
 tccttcactc tgagttggaa agattactct actgaatctc aacctgggtt tatacaaggg 720  
 taccatgtct atctgaaatc caaggcgagg cagtgc 756

<210> 91  
 <211> 58  
 <212> PRT  
 <213> Homo sapiens

<400> 91  
 Arg Lys Lys Thr Gly Tyr Ser Gln Glu Leu Ala Pro Ser Asp Asn Pro  
 1 5 10 15  
 His Val Leu Val Asp Thr Leu Thr Ser His Ser Phe Thr Leu Ser Trp  
 20 25 30  
 Lys Asp Tyr Ser Thr Glu Ser Gln Pro Gly Phe Ile Gln Gly Tyr His  
 35 40 45  
 Val Tyr Leu Lys Ser Lys Ala Arg Gln Cys  
 50 55

<210> 92  
 <211> 79  
 <212> DNA  
 <213> Homo sapiens

<400> 92  
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 aaaaaaaaaa aaaaaaaaaa 79

<210> 93



&lt;211&gt; 1939

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 93

```

attgggttttc aaatattaaa ccagcatttt attttaaaat aaacccact tagttatgat 60
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catcatgttc tttttctgaa attttatttt gttctaagt cataaaataa gttggaaatt 180
atcctctcta tctctacttt gtgaaagaat ttatattaca ttggtattat ttcttccttg 240
aatgtttgat agactatact agtgaaagca tctgggccta gggttttctc tgtggaagat 300
tttcagttac aaattcaatt ttactgagtc aggtttgata agttacattt ctcaaggaat 360
ttatctattt aatcattgaa tgtattgaac attcatttgt ttataatttt gttttgttat 420
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cacctttatt aatcttttca gagaaccact ttttatttct ttgatttcct ttattgtttg 600
ttaacttttt agtttattga tccctctctt tagctttatt acttcccttc ttctacttag 660
taagagttta atttgccctc atttttttag ctctttaagg taggaaattt gattatattt 720
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aaaaaaaaa aaaaaaaaaa

```

1939

&lt;210&gt; 94

&lt;211&gt; 52

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 94

```

Met Ser Val Arg Phe Ile Val Met Phe Pro Phe Leu Phe Leu Thr Leu
 1             5             10            15

Leu Ile Cys Val Leu Ser Pro Ser Ile Pro Leu Ser Leu Ser Leu Val
 20             25            30

Ser Trp Ser Val Gly Leu Ser Pro Leu Leu Ile Phe Ser Glu Asn His
 35             40            45

Phe Leu Phe Leu
 50

```

&lt;210&gt; 95

&lt;211&gt; 1252

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 95

```

gtagaaatcc caaaaagatt tggacagagg cagagcctat gtcactacac cttaaaggat 60
aacaagggtt' atatcaagac tcatgggtgaa catgtaggtt ttagaatttt catggatgcc 120
atactacttt ctttgactag aaagggtgaag atgccagatg tggagctctt tgttaatttg 180
ggagactggc ctttgaaaaa aaagaaatcc aattcaaaca tccatccgat cttttcctgg 240
tgtggctcca cagattccaa ggatatcgtg atgcctacgt acgatttgac tgattctgtt 300
ctggaaacca tgggcccggg aagtctggat atgatgtccg tgcaagctaa cacgggtcct 360
ccctgggaaa gcaaaaattc cactgccgtc tggagagggc gagacagccg caaagagaga 420
ctcgagctgg ttaaaactcag tagaaaacac ccagaactca tagacgctgt tttcaccaac 480
tttttcttct ttaaacacga tgaaaacctg tatggtccca ttgtgaaaca tatttcattt 540
tttgatttct tcaagcataa gtatcaaata aatatcgatg gcactgtagc agcttatcgc 600
ctgccatatt tgctagtggg tgacagtgtt gtgctgaagc aggattccat ctactatgaa 660
catttttata atgagctgca gccctggaaa cactacattc cagttaagag caacctgagc 720
gatctgctag aaaaaactta atgggcgaaa gatcacgatg aagaggccaa aaagatagca 780
aaagcaggac aagaatttgc aagaaataat ctcatgggcg atgacatatt ctgttattat 840
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tctgtgtgat tgtttgcagt atgaagacac atttctactt atgcagtatt ctcagtactg 1140
tactttaaag tacattttta gaattttata ataaaaccac ctttatttta aaggaaaaaa 1200
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 1252

```

&lt;210&gt; 96

&lt;211&gt; 289

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 96

```

Met Asp Ala Ile Leu Leu Ser Leu Thr Arg Lys Val Lys Met Pro Asp
  1             5             10             15

```

```

Val Glu Leu Phe Val Asn Leu Gly Asp Trp Pro Leu Glu Lys Lys Lys
      20             25             30

```

```

Ser Asn Ser Asn Ile His Pro Ile Phe Ser Trp Cys Gly Ser Thr Asp
      35             40             45

```

```

Ser Lys Asp Ile Val Met Pro Thr Tyr Asp Leu Thr Asp Ser Val Leu
      50             55             60

```

```

Glu Thr Met Gly Arg Val Ser Leu Asp Met Met Ser Val Gln Ala Asn
      65             70             75             80

```

```

Thr Gly Pro Pro Trp Glu Ser Lys Asn Ser Thr Ala Val Trp Arg Gly
      85             90             95

```

```

Arg Asp Ser Arg Lys Glu Arg Leu Glu Leu Val Lys Leu Ser Arg Lys
      100            105            110

```

```

His Pro Glu Leu Ile Asp Ala Ala Phe Thr Asn Phe Phe Phe Phe Lys
      115            120            125

```

```

His Asp Glu Asn Leu Tyr Gly Pro Ile Val Lys His Ile Ser Phe Phe
      130            135            140

```

```

Asp Phe Phe Lys His Lys Tyr Gln Ile Asn Ile Asp Gly Thr Val Ala

```

145                      150                      155                      160  
 Ala Tyr Arg Leu Pro Tyr Leu Leu Val Gly Asp Ser Val Val Leu Lys  
                          165                                      170                                      175  
 Gln Asp Ser Ile Tyr Tyr Glu His Phe Tyr Asn Glu L u Gln Pro Trp  
                          180                                      185                                      190  
 Lys His Tyr Ile Pro Val Lys Ser Asn Leu Ser Asp Leu Leu Glu Lys  
                          195                                      200                                      205  
 Leu Lys Trp Ala Lys Asp His Asp Glu Glu Ala Lys Lys Ile Ala Lys  
                          210                                      215                                      220  
 Ala Gly Gln Glu Phe Ala Arg Asn Asn Leu Met Gly Asp Asp Ile Phe  
                          225                                      230                                      235                                      240  
 Cys Tyr Tyr Phe Lys Leu Phe Gln Glu Tyr Ala Asn Leu Gln Val Ser  
                          245                                      250                                      255  
 Glu Pro Gln Ile Arg Glu Gly Met Lys Arg Val Glu Pro Gln Thr Glu  
                          260                                      265                                      270  
 Asp Asp Leu Phe Pro Cys Thr Cys His Arg Lys Lys Thr Lys Asp Glu  
                          275                                      280                                      285

Leu

<210> 97  
 <211> 492  
 <212> DNA  
 <213> Homo sapiens

<400> 97  
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 agagataaaa tgagaaaatg gagagaagaa aactcaagaa atagttagca aattgtggaa 120  
 gttggagaag aattaattaa tgaatatgct tctaagctgg gagatgatat ttggatcata 180  
 tatgaacagg tgatgattgc agcactagac tatggtcggg atgacttggc attgttttgt 240  
 cttcaagagc tgagaagaca gttccctggc agtcacagag tcaagcgatt aacaggcatg 300  
 agatttgaag ccatggaaag atatgatgat gctatacagc tatatgatag gattttacaa 360  
 gaagatccaa ctaacactgc tgcaagaaag cgtaagattg ccattcgaaa agcccagggg 420  
 aaaaatgtgg aggccattcg ggagctgaat gagtatctgg aacaatttgt tggagaccaa 480  
 gaagcctggc at 492

<210> 98  
 <211> 159  
 <212> PRT  
 <213> Homo sapiens

<400> 98  
 Met Ala Lys Val Ser Glu Leu Tyr Asp Val Thr Trp Glu Glu Met Arg  
   1                      5                      10                      15  
 Asp Lys Met Arg Lys Trp Arg Glu Glu Asn Ser Arg Asn Ser Glu Gln  
                          20                                      25                                      30  
 Ile Val Glu Val Gly Glu Glu Leu Ile Asn Glu Tyr Ala Ser Lys Leu  
                          35                                      40                                      45

Gly Asp Asp Il Trp Ile Ile Tyr Glu Gln Val Met Ile Ala Ala Leu  
 50 55 60  
 Asp Tyr Gly Arg Asp Asp Leu Ala Leu Phe Cys Leu Gln Glu Leu Arg  
 65 70 75 80  
 Arg Gln Phe Pro Gly Ser His Arg Val Lys Arg Leu Thr Gly Met Arg  
 85 90 95  
 Phe Glu Ala Met Glu Arg Tyr Asp Asp Ala Ile Gln Leu Tyr Asp Arg  
 100 105 110  
 Ile Leu Gln Glu Asp Pro Thr Asn Thr Ala Ala Arg Lys Arg Lys Ile  
 115 120 125  
 Ala Ile Arg Lys Ala Gln Gly Lys Asn Val Glu Ala Ile Arg Glu Leu  
 130 135 140  
 Asn Glu Tyr Leu Glu Gln Phe Val Gly Asp Gln Glu Ala Trp His  
 145 150 155

<210> 99  
 <211> 85  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (20)

<220>  
 <221> unsure  
 <222> (27)

<400> 99  
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 aaaaaaaaaa aaaaaaaaaa aaaaaa 85

<210> 100  
 <211> 313  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (68)

<220>  
 <221> unsure  
 <222> (108)

<220>  
 <221> unsure  
 <222> (137)

<220>  
 <221> unsure  
 <222> (288)

&lt;400&gt; 100

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atccttcttt gaaaatnaat atggtaactt aaatatattt agtacattac gttcctcttg 180
cttgatcgga catcattcaa aagctcttca aagcatttgt tcaaatcttc agtactggcc 240
agttttcata cagtctcggg gttttaaaac tttgaaatca aggacacnac gtctccagtc 300
tacctccgag aga                                     313

```

&lt;210&gt; 101

&lt;211&gt; 964

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (395)

&lt;400&gt; 101

```

gcttttccgg agcagagttg gagaatcttg tgaaccaggc tgcattaaaa gcagctgttg 60
atggaaaaga aatggttacc atgaaggagc tggagttttc caaagacaaa attctaattg 120
ggcctgaaag aagaagtgtg gaaattgata aaaaaacaa aaccatcaca gcatatcatg 180
aatctgggtca tgccattatt gcatattaca caaaagatgc aatgcctatc aacaaagcta 240
caatcatgcc acggggggcca acacttggac atgtgtccct gttacctgag aatgacagat 300
ggaatgaaac tagagcccag ctgcttgcac aaatggatgt tagtatggga ggaagagtgg 360
cagaggagct tatatttga accgaccata ttacnacagg tgcttccagt gattttgata 420
atgccactaa aatagcaaaag cggatrgyta ccaaatttgg aatgagtga aagcttggag 480
ttatgacctc cagtataca ggggaaacta agtccagaaa cccaatctgc catcgaacaa 540
gaaataagaa tccttctaag ggactcatat gaacgagcaa aacatatctt gaaaactcat 600
gcaaaggagc ataagaatct cgcagaagct ttattgacct atgagacttt ggatgccaaa 660
gagattcaaa ttgttctkga ggggaaaaag ttggaagtga gatgataact ctctkgatat 720
ggatgcttgc tggttttatt gcaagaatat aagtagcatt gcagtagtct acttttacia 780
cgctttcccc tcattcttga tgtggtgtaa ttgaagggtg tgaatgctt tgtcaatcat 840
ttgtcacatt tatccagttt gggttattct cattaggaca cctattgcaa attagcatcc 900
catggcaaat atattttgaa aaaataaaga actatcagga ttgaaaaaaa aaaaaaaaaa 960
aaaa                                             964

```

&lt;210&gt; 102

&lt;211&gt; 166

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (125)..(126)

&lt;400&gt; 102

```

Met Val Thr Met Lys Glu Leu Glu Phe Ser Lys Asp Lys Ile Leu Met
  1                      5                      10                      15

```

```

Gly Pro Glu Arg Arg Ser Val Glu Ile Asp Asn Lys Asn Lys Thr Ile
                20                      25                      30

```

```

Thr Ala Tyr His Glu Ser Gly His Ala Ile Ile Ala Tyr Tyr Thr Lys
    35                      40                      45

```

```

Asp Ala Met Pro Ile Asn Lys Ala Thr Ile Met Pro Arg Gly Pro Thr
    50                      55                      60

```

```

Leu Gly His Val Ser Leu Leu Pro Glu Asn Asp Arg Trp Asn Glu Thr

```

<400> 104  
Met Pro Val Ala Thr Glu Leu Val Ile Val Ser Arg Ile Tyr Gln Tyr  
1 5 10 15

Ile Glu Gln Ile Ile Met Phe Cys Phe Val Leu Phe Leu Phe Leu Tyr  
                   20                  25                  30

Phe Arg Asn Ser Thr Ala Thr Tyr Lys Ser Ser Leu Glu Leu Ser Gly  
           35                  40                  45

Tyr Leu Lys Ser Glu Ala Ser Thr Phe Leu Arg Thr Lys His Arg Asn  
       50                  55                  60

Asp Glu Met Ser Tyr Lys Tyr Pro Phe Ile Leu Phe His Asn Thr Tyr  
       65                  70                  75                  80

Ile Asp Leu Leu Tyr Val  
                   85

<210> 105  
 <211> 479  
 <212> DNA  
 <213> Homo sapiens

<400> 105  
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 cccaaccttt gtccctccca ctcttcgctc gcgcggcggt ctgagaccac caggaccagt 180  
 ttcaggggtt tccttctcca gcgagacttg gcagaacagg ctttaaaagc aaaggaggca 240  
 gcggaagact gtgaattcct ttggacaatt gatgatattt atcattgtgc ccagtttcta 300  
 caaataaaaag atgggtggat tattttctcg atggaggaca aaaccttcaa ctgtagaagt 360  
 tctagaaaagt atagataagg aaattcaagc attggaagaa tttagggaaa aaaaaaaaaa 420  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 479

<210> 106  
 <211> 33  
 <212> PRT  
 <213> Homo sapiens

<400> 106  
 Met Gly Gly Leu Phe Ser Arg Trp Arg Thr Lys Pro Ser Thr Val Glu  
       1                  5                  10                  15

Val Leu Glu Ser Ile Asp Lys Glu Ile Gln Ala Leu Glu Glu Phe Arg  
           20                  25                  30

Glu

<210> 107  
 <211> 333  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (70)

<220>  
 <221> unsure  
 <222> (156)

<220>  
 <221> unsure  
 <222> (184)

<220>  
 <221> unsure  
 <222> (207)

<220>  
 <221> unsure  
 <222> (308)

<400> 107  
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 agtggagaga ggccactccc tctccagccc ccgatntgga cccgggggag gggaggctga 180  
 tgcntttggc cccggcctgg ccaaaanagc ccateccccag ggcagtttca ggtgccggct 240  
 gggccctgaa tgtcaaggat aatatatagc ccgctcctgg gtccctggagc tgtggccctt 300  
 tgtactcntg ttgtgtccat tgtgtgtgtg cgt 333

<210> 108  
 <211> 611  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (62)

<220>  
 <221> unsure  
 <222> (185)

<220>  
 <221> unsure  
 <222> (192)

<220>  
 <221> unsure  
 <222> (249)

<220>  
 <221> unsure  
 <222> (290)

<400> 108  
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 gggctgagtg gggtcgggtg aggcagaggt cagaaacaga agagctgcag ttgctggagc 180  
 tgggntgaga antgggctgc ctctgccat ccccccgtct cctccccctt tcccccttgg 240  
 gccccctnt gctcagaatc tgaagtagtt ccctcctcag caatttcatn tcttgaacac 300  
 tgactcacac ctttttaggca cctactgtgt gcatagcatt ccaccaggac tcatctccct 360  
 tccttctcag ggggtcccga gccccgacta gctttgccct aactccttca tcaaaagacc 420  
 ccccgccagc ttcccacacc tcatacgcag ccacatctgc cctattctcc atgctttcca 480  
 gcttgccctg ccttcctcat ctctccctgc ctgtgcagac ctccaccctt ctttcctcca 540  
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 ctgatcgtcc a 611

<210> 109  
 <211> 47



&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 109

Met Leu Ser Ser Leu Pro Ala Leu Pro His Leu Ser Leu Pro Val Gln  
 1 5 10 15

Thr Ser Thr Leu Leu Ser Ser Thr Pro Pro Ser Pro Asn Ala Cys Arg  
 20 25 30

Pro Ser Ile His Ser Val Ser Ser Cys Val Val Ser Asp Arg Pro  
 35 40 45

&lt;210&gt; 110

&lt;211&gt; 274

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 110

atccagggcg tggggagacc attggcattt gggaaccatt ttccttcgaa cggcttcccc 60  
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 tctgaaatta aatcgcacac cccaccatt tcctctcccc tgggatctgg aggaacatca 180  
 tacatagtag gtgaatcgtt ttgtagagtg aagaatgcta atgtaaagca aatagtcacc 240  
 cacgttcctt tgtaaattca aaaaaaaaaa aaaa 274

&lt;210&gt; 111

&lt;211&gt; 1646

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 111

catcgggtgg actagctggg atctccgcat tggatttggg gctgattacc actgcttgcc 60  
 tattattatt gttgttgtta ctactattat ttttttttac ccaagggaga aagacaaaaa 120  
 aacgggtggga tttatttaac atgatcttgg caaacgtctt ctgctcttcc ttctttctag 180  
 acgagaccct ccgctctttg gccagccctt cctccctgca gggccccgag ctccacggct 240  
 ggcgcccccc agtggactgt gtccgggcca atgagctgtg tgccgcccga tccaactgca 300  
 gctctcgcta ccgcactctg cggcagtgcg tggcaggccg cgaccgcaac accatgctgg 360  
 ccaacaagga gtgccaggcg gccttggagg tcttgaggga gagcccgctg tacgactgcc 420  
 gctgcaagcg gggcatgaag aaggagctgc agtgctctgca gatctactgg agcatccacc 480  
 tggggctgac cgagggtgag gagttctacg aagcctcccc ctatgagccg gtgacctccc 540  
 gcctctcgga catcttcagg cttgcttcaa tcttctcagg gacaggggca gaccggtgg 600  
 tcagcgccaa gagcaaccat tgcttggatg ctgccaaggc ctgcaacctg aatgacaact 660  
 gcaagaagct gcgctcctcc tacatctcca tctgcaaccg cgagatctcg cccaccgagc 720  
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 acaaggtgat caaacctaac tcaggcccca gcagagccag accgtcggct gccttgaccg 1500  
 tgctgtctgt cctgatgctg aaacaggcct tgtaggctgt gggaaccgag tcagaagatt 1560  
 tttgaaagct acgcagacaa gaacagccgc ctgacgaaat ggaaacacac acagacacac 1620  
 acacaccttg caaaaaaaaaa aaaaaa 1646

&lt;210&gt; 112

&lt;211&gt; 464

&lt;212&gt; PRT

&lt;213&gt; H m sapiens

&lt;400&gt; 112

Met Ile Leu Ala Asn Val Phe Cys Leu Phe Phe Phe Leu Asp Glu Thr  
 1 5 10 15

Leu Arg Ser Leu Ala Ser Pro Ser Ser Leu Gln Gly Pro Glu Leu His  
 20 25 30

Gly Trp Arg Pro Pro Val Asp Cys Val Arg Ala Asn Glu Leu Cys Ala  
 35 40 45

Ala Glu Ser Asn Cys Ser Ser Arg Tyr Arg Thr Leu Arg Gln Cys Leu  
 50 55 60

Ala Gly Arg Asp Arg Asn Thr Met Leu Ala Asn Lys Glu Cys Gln Ala  
 65 70 75 80

Ala Leu Glu Val Leu Gln Glu Ser Pro Leu Tyr Asp Cys Arg Cys Lys  
 85 90 95

Arg Gly Met Lys Lys Glu Leu Gln Cys Leu Gln Ile Tyr Trp Ser Ile  
 100 105 110

His Leu Gly Leu Thr Glu Gly Glu Glu Phe Tyr Glu Ala Ser Pro Tyr  
 115 120 125

Glu Pro Val Thr Ser Arg Leu Ser Asp Ile Phe Arg Leu Ala Ser Ile  
 130 135 140

Phe Ser Gly Thr Gly Ala Asp Pro Val Val Ser Ala Lys Ser Asn His  
 145 150 155 160

Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asn Asp Asn Cys Lys Lys  
 165 170 175

Leu Arg Ser Ser Tyr Ile Ser Ile Cys Asn Arg Glu Ile Ser Pro Thr  
 180 185 190

Glu Arg Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe  
 195 200 205

Asp Arg Val Pro Ser Glu Tyr Thr Tyr Arg Met Leu Phe Cys Ser Cys  
 210 215 220

Gln Asp Gln Ala Cys Ala Glu Arg Arg Arg Gln Thr Ile Leu Pro Ser  
 225 230 235 240

Cys Ser Tyr Glu Asp Lys Glu Lys Pro Asn Cys Leu Asp Leu Arg Gly  
 245 250 255

Val Cys Arg Thr Asp His Leu Cys Arg Ser Arg L u Ala Asp Phe His  
 260 265 270

Ala Asn Cys Arg Ala Ser Tyr Gln Thr Val Thr Ser Cys Pro Ala Asp  
 275 280 285

Asn Tyr Gln Ala Cys Leu Gly Ser Tyr Ala Gly Met Ile Gly Phe Asp  
 290 295 300  
 Met Thr Pro Asn Tyr Val Asp Ser Ser Pro Thr Gly Il Val Val Ser  
 305 310 315 320  
 Pro Trp Cys Ser Cys Arg Gly Ser Gly Asn Met Glu Glu Glu Cys Glu  
 325 330 335  
 Lys Phe Leu Arg Asp Phe Thr Glu Asn Pro Cys Leu Arg Asn Ala Ile  
 340 345 350  
 Gln Ala Phe Gly Asn Gly Thr Asp Val Asn Val Ser Pro Lys Gly Pro  
 355 360 365  
 Ser Phe Gln Ala Thr Gln Ala Pro Arg Val Glu Lys Thr Pro Ser Leu  
 370 375 380  
 Pro Asp Asp Leu Ser Asp Ser Thr Ser Leu Gly Thr Ser Val Ile Thr  
 385 390 395 400  
 Thr Cys Thr Ser Val Gln Glu Gln Gly Leu Lys Ala Asn Asn Ser Lys  
 405 410 415  
 Glu Leu Ser Met Cys Phe Thr Glu Leu Thr Thr Asn Ile Ile Pro Gly  
 420 425 430  
 Ser Asn Lys Val Ile Lys Pro Asn Ser Gly Pro Ser Arg Ala Arg Pro  
 435 440 445  
 Ser Ala Ala Leu Thr Val Leu Ser Val Leu Met Leu Lys Gln Ala Leu  
 450 455 460

<210> 113  
 <211> 355  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (133)

<220>  
 <221> unsure  
 <222> (151)

<220>  
 <221> unsure  
 <222> (196)

<220>  
 <221> unsure  
 <222> (228)

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 tcttaaggaa acngacgtgc tcttctccgt ntaccagcac tcgggcccgc gagatccagt 180

cctgaggctt caccntgga acaactgcac gcccctcaat cttgaagnga tctcctatgc 240  
 cgacccact ccctccgat ccctcagcag cagccccggg cacctccgag ttctggacat 300  
 ccccgatag cagcagcagc agcaggacgg gaaagaagcc ccacagagcg gccgc 355

<210> 114

<211> 587

<212> DNA

<213> Homo sapiens

<400> 114

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 cagtcaatga atatgctgaa ttccaacat gagttgcctg atgtttctga gttcatgaca 180  
 agactcttct cttcaaaatc atctggcaaa tctagcagcg gcagcagtaa aacaggcaaa 240  
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 caacactggg tggcatccaa gtcttggaac accgtgtgaa gcaactacta taaacttgag 360  
 tcatcccgac gttgatctct tacaactgtg tatgttaact ttttagcaca tgtttgttac 420  
 ttggtacacg agaaaaccca gctttcatct tttgtctgta tgaggtaaat attgatgtca 480  
 ctgaattaat tacagtgtcc tatagaaaat gccattaata aattatatga actactatac 540  
 attatgtata ttaattaaaa catcttaatc cagaaaaaaa aaaaaaa 587

<210> 115

<211> 81

<212> PRT

<213> Homo sapiens

<400> 115

Met Asn Pro Met Val Met Met Met Val Leu Pro Leu Leu Ile Phe Val  
 1 5 10 15

Leu Leu Pro Lys Val Val Asn Thr Ser Asp Pro Asp Met Arg Arg Glu  
 20 25 30

Met Glu Gln Ser Met Asn Met Leu Asn Ser Asn His Glu Leu Pro Asp  
 35 40 45

Val Ser Glu Phe Met Thr Arg Leu Phe Ser Ser Lys Ser Ser Gly Lys  
 50 55 60

Ser Ser Ser Gly Ser Ser Lys Thr Gly Lys Ser Gly Ala Gly Lys Arg  
 65 70 75 80

Arg

<210> 116

<211> 601

<212> DNA

<213> Homo sapiens

<400> 116

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 gcagtacgtg atcggcctgt tcctctctgt cctctacacc atcttctctt tccccatcgg 180  
 ctttgtgggc aacatcctga tcctgggtgg gaacatcagc ttccgcgaga agatgacct 240  
 ccccgacctg tacttcatca acctggcggt ggccggacct atcctgggtg ccgactccct 300  
 cattgagggt ttcaacctgc acgagcggta ctacgacatc gccgtcctgt gcaccttcat 360  
 gtcgctcttc ctgcaggta acatgtacag cagcgtcttc ttctcacct ggatgagctt 420  
 cgaccgctac atcgccctgg ccagggccat gcgctgcagc ctgttccgca ccaagcacca 480

cgcccggtg agctgtggcc tcattctggat ggcattcgtg tcagccacgc tggtagccctt 540  
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 g 601

<210> 117  
 <211> 200  
 <212> PRT  
 <213> Homo sapiens

<400> 117

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Glu	Leu	Asn	Leu	Ser	His	Pro	Leu	Leu	Gly	Thr	Ala	Leu	Ala	Asn	Gly
		20						25					30		
Thr	Gly	Glu	Leu	Ser	Glu	His	Gln	Gln	Tyr	Val	Ile	Gly	Leu	Phe	Leu
	35						40					45			
Ser	Cys	Leu	Tyr	Thr	Ile	Phe	Leu	Phe	Pro	Ile	Gly	Phe	Val	Gly	Asn
	50					55					60				
Ile	Leu	Ile	Leu	Val	Val	Asn	Ile	Ser	Phe	Arg	Glu	Lys	Met	Thr	Ile
65					70					75					80
Pro	Asp	Leu	Tyr	Phe	Ile	Asn	Leu	Ala	Val	Ala	Asp	Leu	Ile	Leu	Val
				85					90					95	
Ala	Asp	Ser	Leu	Ile	Glu	Val	Phe	Asn	Leu	His	Glu	Arg	Tyr	Tyr	Asp
		100						105					110		
Ile	Ala	Val	Leu	Cys	Thr	Phe	Met	Ser	Leu	Phe	Leu	Gln	Val	Asn	Met
	115						120					125			
Tyr	Ser	Ser	Val	Phe	Phe	Leu	Thr	Trp	Met	Ser	Phe	Asp	Arg	Tyr	Ile
	130					135					140				
Ala	Leu	Ala	Arg	Ala	Met	Arg	Cys	Ser	Leu	Phe	Arg	Thr	Lys	His	His
145					150					155					160
Ala	Arg	Leu	Ser	Cys	Gly	Leu	Ile	Trp	Met	Ala	Ser	Val	Ser	Ala	Thr
			165						170					175	
Leu	Val	Pro	Phe	Thr	Ala	Val	His	Leu	Gln	His	Thr	Asp	Glu	Ala	Cys
		180						185					190		
Phe	Cys	Phe	Ala	Asp	Val	Arg	Glu								
	195					200									

<210> 118  
 <211> 419  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (80)

<220>

&lt;221&gt; unsure

&lt;222&gt; (178)

&lt;400&gt; 118

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gccgtctgct ccgggggtggt tcagtcactg cttgttgaca tcaacatggc aattgcantc 180
atgtggactg ggaccgtgcg agctgccgtg tgggttagtc gggtgccagg acaatgaaat 240
actccagcac gtgtggctga cgaatttggt ttacagaaa taacagctgg ggacaactgc 300
gggtgatgatg taaaaacctt ccataaaaat gtaagaaaag ctgatgaggg tggtgacgtt 360
cagcctttgt caataaacct gtcattgtgcg gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 419

```

&lt;210&gt; 119

&lt;211&gt; 714

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (646)

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (649)

&lt;400&gt; 119

```

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tatctttctg cctcaagtac tggatgtgtt ttatgccaac atgaagaaaa gagaagggac 180
tcagctttct tccaacagay ctartswtst ytwmyttky akcatttttg ggcttttcaa 240
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ttcgggtgtg tggtgaaaat gtcacgtgtg tggaatacgc tatctcctgg ctacaagacc 360
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atgaaattga ggcgatgatc aagagagttc gattggccaa agaacaggaa tcccgggcag 600
attgtatcag tgagtttata gaatggcagt ataatgacaa taacanttnt cattgtttta 660
acaaaatgac caatctgaaa ttagaggatg caaggagaga aaaaaaaaaa aaaa 714

```

&lt;210&gt; 120

&lt;211&gt; 159

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (141)..(142)

&lt;400&gt; 120

```

Phe Leu Gly Phe Ser Lys Gln Ser Pro Gln Lys Lys Asn His Leu Val
  1             5             10            15

```

```

Leu Glu Lys Lys Thr Glu Ser Ala Thr Phe Arg Val Cys Gly Glu Asn
      20             25            30

```

```

Val Thr Cys Val Glu Tyr Ala Ile Ser Trp Leu Gln Asp Leu Ile Glu
    35             40            45

```

```

Lys Glu Gln Cys Pro Tyr Thr Ser Glu Asp Glu Cys Ile Lys Asp Phe
    50             55            60

```

Asp Glu Lys Glu Tyr Gln Glu Leu Asn Glu Leu Gln Lys Lys Leu Asn  
65 70 75 80

Ile Asn Ile Ser Leu Asp His Lys Arg Pro Leu Ile Lys Val Leu Gly  
85 90 95

Ile Ser Arg Asp Val Met Gln Ala Arg Asp Glu Ile Glu Ala Met Ile  
100 105 110

Lys Arg Val Arg Leu Ala Lys Glu Gln Glu Ser Arg Ala Asp Cys Ile  
115 120 125

Ser Glu Phe Ile Glu Trp Gln Tyr Asn Asp Asn Asn Xaa Xaa His Cys  
130 135 140

Phe Asn Lys Met Thr Asn Leu Lys Leu Glu Asp Ala Arg Arg Glu  
145 150 155

<210> 121

<211> 2681

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (2656)

<400> 121

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catgtgcccga cctttcctgt ctcttttact ttgcagcacc aaatgctttc tactttgtgg 180  
tctaggaggga acacatgtca cttttgtaag ctgctcgaaa gcaggggcca caccttcac 240  
cttgttttcc acacaacacc aagcacttag tagacaccca ataaatcatt gctgaatgaa 300  
tgtattcagc ctggaattgc actaggattt ttgggccaac acattgtatt cttactgat 360  
accagacttc caatcaaata aaatccttaa gccttttcca tagtcttta ttaactact 420  
tctcttccat tatttccctt tgctacttt tgaactgata ttcagaactt ttctgttaat 480  
gtttaatttt catccattat tcttgtctgt acagatcttt ttgatttttg actctcttat 540  
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ttgactatcg ttcatgaag ttgttgatac aaatgttgaa caggagaaaa accagtagct 660  
tgccaacttg gcacctcatt ctctagcttg acagtaatct ctatctagt agtttttaga 720  
tatggttatt taatcaaata tctactagct ctaattttgt tataattcat tcatgtatac 780  
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ccacaccag cagaagaac tctaggaaat atggtcttat gctaggtaac cccaaacca 1740  
gctaaaactg ttgcttttga agaagggtga aacagacaat gtggaggaga attaccagtc 1800

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```

&lt;210&gt; 122

&lt;211&gt; 132

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 122

```

Met Glu Ala Val Arg Met Asn Trp Lys Glu Arg Leu Trp Glu Arg Gln
  1             5             10             15

```

```

Arg Asp Glu Asn Lys Pro Gly Leu Ala Leu Pro Cys Ala His Thr Gly
          20             25             30

```

```

Glu Leu Cys Ala Pro Gly Cys Val Ser Trp Tyr Met Arg Leu Ser Glu
          35             40             45

```

```

Gly Ser Trp Gly Ala Leu Leu Ala Gln Arg Leu Arg Gly Arg Pro Arg
          50             55             60

```

```

Lys Pro Phe Phe Ala Leu Val Arg Val Cys Cys Ile Phe Pro Ser Pro
          65             70             75             80

```

```

Gly Asn Gly Thr Gln Phe Phe Phe Phe Leu Cys Lys Ile Ile Ser Ile
          85             90             95

```

```

Thr Ile Gly Cys Ala His Glu Asn Ala Phe Cys Phe His Arg Asn Val
          100            105            110

```

```

Phe Ser His Ser Val Leu Ile Leu Ile Ser Val Lys Leu Ser Lys His
          115            120            125

```

```

Ile Thr Lys Phe
          130

```

&lt;210&gt; 123

&lt;211&gt; 1585

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 123

```

ctaagctatt tgattctagg tctagaatgt tatctcttat tagaggatat gtttaatttc 60
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tactaaggat tgaggacca aagatgaaca aaacatgggg cctaattcaa agatttcaca 180
atctggagag aaagtcagcc acatacaaaa aattataagg tagaatgtgc tataaaaaat 240

```



```

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ttgaaacagt aaaaaaaaaa aaaaa 1585

```

&lt;210&gt; 124

&lt;211&gt; 63

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 124

```

Met Leu Ser Leu Ile Arg Gly Tyr Val Asn Phe Pro Ala Phe Tyr Ser
 1             5             10             15

```

```

Phe Ile Asn Leu Thr Ser Leu Ile Ala Tyr His Val Ser Gly Ser Val
      20             25             30

```

```

Leu Arg Ile Glu Asp Pro Lys Met Asn Lys Thr Trp Gly Leu Ile Gln
      35             40             45

```

```

Arg Phe His Asn Leu Glu Arg Lys Ser Ala Thr Tyr Lys Lys Leu
      50             55             60

```

&lt;210&gt; 125

&lt;211&gt; 625

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 125

```

gatccacca gttctgcctg gtttctcca tccccagagg cactaaaagc agtattttta 60
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aactagggga cagaggttct tatttgcga ttttatttta taatttgacc acagcatctg 180
aactccctct ctccctggaa taagtatttt tcccacattt ttggatata gtatggtaga 240
caattttttt ttaagacaca gagataaatg ttttcctgct ttggttacct ttcctttccc 300
ctttaaagg aattagctat agaactgctt tgtaaagatg cttcttgata ttttactttt 360
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tagcttatga tatttgctgc cgagatgta taacaaggac tcgttcatgt atataagcta 540
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aaaaaaaaa aaaaaaaaaa aaaaa 625

```

<210> 126  
 <211> 24  
 <212> PRT  
 <213> Homo sapiens

<400> 126  
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 Phe Ser Pro Leu Leu Gln Lys Ala  
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<210> 127  
 <211> 1946  
 <212> DNA  
 <213> Homo sapiens

<400> 127  
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<210> 128  
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 <212> PRT  
 <213> Homo sapiens

<220>

&lt;221&gt; UNSURE

&lt;222&gt; (83)

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (480)

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (482)

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (490)

&lt;400&gt; 128

Met Lys Pro Lys Leu Met Tyr Gln Glu Leu Lys Val Pro Ala Glu Glu  
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Pro Ala Asn Glu Leu Pro Met Asn Glu Ile Glu Ala Trp Lys Ala Ala  
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Glu Lys Lys Ala Arg Trp Val Leu Leu Val Leu Ile Leu Ala Val Val  
 35 40 45

Gly Phe Gly Ala Leu Met Thr Gln Leu Phe Leu Trp Glu Tyr Gly Asp  
 50 55 60

Leu His Leu Phe Gly Pro Asn Gln Arg Pro Ala Pro Cys Tyr Asp Pro  
 65 70 75 80

Cys Glu Xaa Val Leu Val Glu Ser Ile Pro Glu Gly Leu Asp Phe Pro  
 85 90 95

Asn Ala Ser Thr Gly Asn Pro Ser Thr Ser Gln Ala Trp Leu Gly Leu  
 100 105 110

Leu Ala Gly Ala His Ser Ser Leu Asp Ile Ala Ser Phe Tyr Trp Thr  
 115 120 125

Leu Thr Asn Asn Asp Thr His Thr Gln Glu Pro Ser Ala Gln Gln Gly  
 130 135 140

Glu Glu Val Leu Arg Gln Leu Gln Thr Leu Ala Pro Lys Gly Val Asn  
 145 150 155 160

Val Arg Ile Ala Val Ser Lys Pro Ser Gly Pro Gln Pro Gln Ala Asp  
 165 170 175

Leu Gln Ala Leu Leu Gln Ser Gly Ala Gln Val Arg Met Val Asp Met  
 180 185 190

Gln Lys Leu Thr His Gly Val Leu His Thr Lys Phe Trp Val Val Asp  
 195 200 205

Gln Thr His Phe Tyr Leu Gly Ser Ala Asn Met Asp Trp Arg Ser Leu  
 210 215 220

Thr Gln Val Lys Glu Leu Gly Val Val Met Tyr Asn Cys Ser Cys Leu  
 225 230 235 240

Ala Arg Asp Leu Thr Lys Ile Phe Glu Ala Tyr Trp Phe Leu Gly Gln  
 245 250 255

Ala Gly Ser Ser Ile Pro Ser Thr Trp Pro Arg Phe Tyr Asp Thr Arg  
 260 265 270

Tyr Asn Gln Glu Thr Pro Met Glu Ile Cys Leu Asn Gly Thr Pro Ala  
 275 280 285

Leu Ala Tyr Leu Ala Ser Ala Pro Pro Pro Leu Cys Pro Ser Gly Arg  
 290 295 300

Thr Pro Asp Leu Lys Ala Leu Leu Asn Val Val Asp Asn Ala Arg Ser  
 305 310 315 320

Phe Ile Tyr Val Ala Val Met Asn Tyr Leu Pro Thr Leu Glu Phe Ser  
 325 330 335

His Pro His Arg Phe Trp Pro Ala Ile Asp Asp Gly Leu Arg Arg Ala  
 340 345 350

Thr Tyr Glu Arg Gly Val Lys Val Arg Leu Leu Ile Ser Cys Trp Gly  
 355 360 365

His Ser Glu Pro Ser Met Arg Ala Phe Leu Leu Ser Leu Ala Ala Leu  
 370 375 380

Arg Asp Asn His Thr His Ser Asp Ile Gln Val Lys Leu Phe Val Val  
 385 390 395 400

Pro Ala Asp Glu Ala Gln Ala Arg Ile Pro Tyr Ala Arg Val Asn His  
 405 410 415

Asn Lys Tyr Met Val Thr Glu Arg Ala Thr Tyr Ile Gly Thr Ser Asn  
 420 425 430

Trp Ser Gly Asn Tyr Phe Thr Glu Thr Ala Gly Thr Ser Leu Leu Val  
 435 440 445

Thr Gln Asn Gly Arg Gly Gly Leu Arg Ser Gln Leu Glu Ala Ile Phe  
 450 455 460

Leu Arg Asp Trp Asp Ser Pro Tyr Ser His Asp Leu Asp Thr Ser Xaa  
 465 470 475 480

Asp Xaa Val Gly Asn Ala Cys Arg Leu Xaa  
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&lt;210&gt; 129

&lt;211&gt; 6254

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 129

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&lt;210&gt; 130

&lt;211&gt; 1192

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 130

Met Gln Leu Asn Ile Met Pro Thr Lys Lys Arg Leu Ser Ala Gly Arg  
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Val Pro Leu Ile Leu Phe Leu Cys Gln Met Ile Ser Ala Leu Glu Val  
20 25 30

Pro Leu Asp Pro Lys Leu Leu Glu Asp Leu Val Gln Pro Pro Thr Ile  
35 40 45

Thr Gln Gln Ser Pro Lys Asp Tyr Ile Ile Asp Pro Arg Glu Asn Ile  
50 55 60

Val Ile Gln Cys Glu Ala Lys Gly Lys Pro Pro Pro Ser Phe Ser Trp  
 65 70 75 80  
 Thr Arg Asn Gly Thr His Phe Asp Ile Asp Lys Asp Pro Leu Val Thr  
 85 90 95  
 Met Lys Pro Gly Thr Gly Thr Leu Ile Ile Asn Ile Met Ser Glu Gly  
 100 105 110  
 Lys Ala Glu Thr Tyr Glu Gly Val Tyr Gln Cys Thr Ala Arg Asn Glu  
 115 120 125  
 Arg Gly Ala Ala Val Ser Asn Asn Ile Val Val Arg Pro Ser Arg Ser  
 130 135 140  
 Pro Leu Trp Thr Lys Glu Lys Leu Glu Pro Ile Thr Leu Gln Ser Gly  
 145 150 155 160  
 Gln Ser Leu Val Leu Pro Cys Arg Pro Pro Ile Gly Leu Pro Pro Pro  
 165 170 175  
 Ile Ile Phe Trp Met Asp Asn Ser Phe Gln Arg Leu Pro Gln Ser Glu  
 180 185 190  
 Arg Val Ser Gln Gly Leu Asn Gly Asp Leu Tyr Phe Ser Asn Val Leu  
 195 200 205  
 Pro Glu Asp Thr Arg Glu Asp Tyr Ile Cys Tyr Ala Arg Phe Asn His  
 210 215 220  
 Thr Gln Thr Ile Gln Gln Lys Gln Pro Ile Ser Val Lys Val Ile Ser  
 225 230 235 240  
 Ala Lys Ser Ser Arg Glu Arg Pro Pro Thr Phe Leu Thr Pro Glu Gly  
 245 250 255  
 Asn Ala Ser Asn Lys Glu Glu Leu Arg Gly Asn Val Leu Ser Leu Glu  
 260 265 270  
 Cys Ile Ala Glu Gly Leu Pro Thr Pro Ile Ile Tyr Trp Ala Lys Glu  
 275 280 285  
 Asp Gly Met Leu Pro Lys Asn Arg Thr Val Tyr Lys Asn Phe Glu Lys  
 290 295 300  
 Thr Leu Gln Ile Ile His Val Ser Glu Ala Asp Ser Gly Asn Tyr Gln  
 305 310 315 320  
 Cys Ile Ala Lys Asn Ala Leu Gly Ala Ile His His Thr Ile Ser Val  
 325 330 335  
 Arg Val Lys Ala Ala Pro Tyr Trp Ile Thr Ala Pro Gln Asn Leu Val  
 340 345 350  
 Leu Ser Pro Gly Glu Asp Gly Thr Leu Ile Cys Arg Ala Asn Gly Asn  
 355 360 365  
 Pro Lys Pro Arg Ile Ser Trp Leu Thr Asn Gly Val Pro Ile Glu Ile  
 370 375 380

Ala Pro Asp Asp Pro Ser Arg Lys Ile Asp Gly Asp Thr Ile Ile Phe  
 385 390 395 400  
 Ser Asn Val Gln Glu Arg Ser Ser Ala Val Tyr Gln Cys Asn Ala Ser  
 405 410 415  
 Asn Glu Tyr Gly Tyr Leu Leu Ala Asn Ala Phe Val Asn Val Leu Ala  
 420 425 430  
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 435 440 445  
 Ala Asn Arg Pro Ala Leu Leu Asp Cys Ala Phe Phe Gly Ser Pro Leu  
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 Pro Thr Ile Glu Trp Phe Lys Gly Ala Lys Gly Ser Ala Leu His Glu  
 465 470 475 480  
 Asp Ile Tyr Val Leu His Glu Asn Gly Thr Leu Glu Ile Pro Val Ala  
 485 490 495  
 Gln Lys Asp Ser Thr Gly Thr Tyr Thr Cys Val Ala Arg Asn Lys Leu  
 500 505 510  
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 515 520 525  
 Ile Val Lys Gln Pro Glu Tyr Ala Val Val Gln Arg Gly Ser Met Val  
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 Ser Phe Glu Cys Lys Val Lys His Asp His Thr Leu Ser Leu Thr Val  
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 580 585 590  
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 Asp Lys Ser Val Gln Leu Ser Trp Thr Pro Gly Asp Asp Asn Asn Ser  
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 Pro Ile Thr Lys Phe Ile Ile Glu Tyr Glu Asp Ala Met His Lys Pro  
 660 665 670  
 Gly Leu Trp His His Gln Thr Glu Val Ser Gly Thr Gln Thr Thr Ala  
 675 680 685  
 Gln Leu Lys Leu Ser Pro Tyr Val Asn Tyr Ser Phe Arg Val Met Ala  
 690 695 700



Val Asn Ser Ile Gly Lys Ser Leu Pro Ser Glu Ala Ser Glu Gln Tyr  
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 725 730 735  
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 740 745 750  
 Gly Phe Glu Ser Asn Gly Pro Gly Leu Gln Tyr Lys Val Ser Trp Arg  
 755 760 765  
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 Ser Lys Tyr Ile Val Ser Gly Thr Pro Thr Phe Val Pro Tyr Leu Ile  
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Ala Val Thr Thr Val Asp Glu Ala Gly Ile Leu Pro Pro Asp Val Gly  
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Ala Gly Lys Ala Met Ala Ser Arg Gln Val Asp Ile Ala Thr Gln Gly  
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Trp Phe Ile Gly Leu Met Cys Ala Val Ala Leu Leu Ile Leu Ile Leu  
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Leu Ile Val Cys Phe Ile Arg Arg Asn Lys Gly Gly Lys Tyr Pro Val  
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Lys Glu Lys Glu Asp Ala His Ala Asp Pro Glu Ile Gln Pro Met Lys  
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Glu Asp Asp Gly Thr Phe Gly Glu Tyr Ser Asp Ala Glu Asp His Lys  
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Pro Leu Lys Lys Gly Ser Arg Thr Pro Ser Asp Arg Thr Val Lys Lys  
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Glu Asp Ser Asp Asp Ser Leu Val Asp Tyr Gly Glu Gly Val Asn Gly  
1140 1145 1150

Gln Phe Asn Glu Asp Gly Ser Phe Ile Gly Gln Tyr Ser Gly Lys Lys  
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Glu Lys Glu Pro Ala Glu Gly Asn Glu Ser Ser Glu Ala Pro Ser Pro  
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Val Asn Ala Met Asn Ser Phe Val  
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<210> 131

<211> 4253

<212> DNA

<213> Homo sapiens

<400> 131

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&lt;210&gt; 132

&lt;211&gt; 479

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (13)..(14)

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (21)

&lt;400&gt; 132

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Leu Phe Gln Met Xaa Gln Ala Pro Val Leu Glu Gly Arg Cys Pro Pro  
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Pro Met Val Gly His Arg Ala Ser Gln Thr Gln Thr Ala Pro Val Glu  
 35 40 45

Glu Ser Asp Phe Asp Thr Met Pro Asp Ile Glu Ser Asp Lys Asn Ile  
 50 55 60

Ile Arg Thr Lys Met Phe Leu Tyr Leu Ser Asp Leu Ser Arg Lys Asp  
 65 70 75 80

Arg Arg Ile Val Ser Lys Lys Tyr Lys Ile Tyr Phe Trp Asn Ile Ile  
 85 90 95

Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Ile Gln Leu Val Ile Thr  
 100 105 110

Tyr Gln Thr Val Val Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr Tyr  
 115 120 125

Asn Phe Leu Cys Ala His Pro Leu Gly Val Leu Ser Ala Phe Asn Asn  
 130 135 140

Ile Leu Ser Asn Leu Gly His Val Leu Leu Gly Phe Leu Phe Leu Leu  
 145 150 155 160

Ile Val Leu Arg Arg Asp Ile Leu His Arg Arg Ala Leu Glu Ala Lys  
 165 170 175

Asp Ile Phe Ala Val Glu Tyr Gly Ile Pro Lys His Phe Gly Leu Phe  
 180 185 190

Tyr Ala Met Gly Ile Ala Leu Met Met Glu Gly Val Leu Ser Ala Cys  
 195 200 205

Tyr His Val Cys Pro Asn Tyr Ser Asn Phe Gln Phe Asp Thr Ser Phe  
 210 215 220

Met Tyr Met Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Thr Arg  
 225 230 235 240

His Pro Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Ser Phe Ala  
 245 250 255

Val Val Ile Met Val Thr Val Leu Gly Val Val Phe Gly Lys Asn Asp  
 260 265 270

Val Trp Phe Trp Val Ile Phe Ser Ala Ile His Val Leu Ala Ser Leu  
 275 280 285

Ala Leu Ser Thr Gln Ile Tyr Tyr Met Gly Arg Phe Lys Ile Asp Val  
 290 295 300

Ser Asp Thr Asp Leu Gly Ile Phe Arg Arg Ala Ala Met Val Phe Tyr  
 305 310 315 320

Thr Asp Cys Ile Gln Gln Cys Ser Arg Pro Leu Tyr Met Asp Arg Met  
 325 330 335

Val Leu Leu Val Val Gly Asn Leu Val Asn Trp Ser Phe Ala Leu Phe  
 340 345 350

Gly Leu Ile Tyr Arg Pro Arg Asp Phe Ala Ser Tyr Met Leu Gly Ile  
 355 360 365

Phe Ile Cys Asn Leu Leu Leu Tyr Leu Ala Phe Tyr Ile Ile Met Lys  
 370 375 380

Leu Arg Ser Ser Glu Lys Val Leu Pro Val Pro Leu Phe Cys Ile Val  
 385 390 395 400

Ala Thr Ala Val Met Trp Ala Ala Ala Leu Tyr Phe Phe Phe Gln Asn  
 405 410 415

Leu Ser Ser Trp Glu Gly Thr Pro Ala Glu Ser Arg Glu Lys Asn Arg  
 420 425 430

Glu Cys Ile Leu Leu Asp Phe Phe Asp Asp His Asp Ile Trp His Phe  
 435 440 445

Leu Ser Ala Thr Ala Leu Phe Phe Ser Phe Leu Val Leu Leu Thr Leu  
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Asp Asp Asp Leu Asp Val Val Arg Arg Asp Gln Ile Pro Val Phe  
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&lt;210&gt; 133

&lt;211&gt; 462

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 133

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&lt;210&gt; 134

&lt;211&gt; 147

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 134

Met Ser Gln Cys Thr Ser Ser Thr Ile Pro Ser Ser Ser Gln Glu Lys  
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Asp Pro Lys Ile Lys Thr Glu Thr Ser Glu Glu Gly Ser Gly Asp Leu  
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 Asp Asn Leu Asp Ala Ile Leu Gly Asp Leu Thr Ser Ser Asp Phe Tyr  
                   35                  40                  45  
 Asn Asn Ser Ile Ser Ser Asn Gly Ser His Leu Gly Thr Lys Gln Gln  
                   50                  55                  60  
 Val Phe Gln Gly Thr Asn Ser Leu Gly Leu Lys Ser Ser Gln Ser Val  
                   65                  70                  75                  80  
 Gln Ser Ile Arg Pro Pro Tyr Asn Arg Ala Val Ser Leu Asp Ser Pro  
                   85                  90                  95  
 Val Ser Val Gly Ser Ser Pro Pro Val Lys Asn Ile Ser Ala Phe Pro  
                   100                  105                  110  
 Met Leu Pro Lys Gln Pro Met Leu Gly Gly Asn Pro Arg Met Met Asp  
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 Ser Lys Ala  
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 <212> DNA  
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<210> 136  
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&lt;210&gt; 137

&lt;211&gt; 547

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 137

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Met Ala Ala Val Ser Leu Arg Leu Gly Asp Leu Val Trp Gly Lys Leu
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Gly Arg Tyr Pro Pro Trp Pro Gly Lys Ile Val Asn Pro Pro Lys Asp
      20             25            30

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Leu Lys Lys Pro Arg Gly Lys Lys Cys Phe Phe Val Lys Phe Phe Gly
  35             40            45

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Thr Glu Asp His Ala Trp Ile Lys Val Glu Gln Leu Lys Pro Tyr His
  50             55            60

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Ala His Lys Glu Glu Met Ile Lys Ile Asn Lys Gly Lys Arg Phe Gln

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Asp Gln Thr Ser	Ser His Asn Ser Ser Asp Asp Lys Asn Arg Arg Asn					
	100		105		110	
Ser Ser Glu Glu Arg Ser Arg Pro Asn Ser Gly Asp Glu Lys Arg Lys						
	115		120		125	
Leu Ser Leu Ser Glu Gly Lys Val Lys Lys Asn Met Gly Glu Gly Lys						
	130		135		140	
Lys Arg Val Ser Ser Gly Ser Ser Glu Arg Gly Ser Lys Ser Pro Leu						
	145		150		155	160
Lys Arg Ala Gln Glu Gln Ser Pro Arg Lys Arg Gly Arg Pro Pro Lys						
	165		170		175	
Asp Glu Lys Asp Leu Thr Ile Pro Glu Ser Ser Thr Val Lys Gly Met						
	180		185		190	
Met Ala Gly Pro Met Ala Ala Phe Lys Trp Gln Pro Thr Ala Ser Glu						
	195		200		205	
Pro Val Lys Asp Ala Asp Pro His Phe His His Phe Leu Leu Ser Gln						
	210		215		220	
Thr Glu Lys Pro Ala Val Cys Tyr Gln Ala Ile Thr Lys Lys Leu Lys						
	225		230		235	240
Ile Cys Glu Glu Glu Thr Gly Ser Thr Ser Ile Gln Ala Ala Asp Ser						
	245		250		255	
Thr Ala Val Asn Gly Ser Ile Thr Pro Thr Asp Lys Lys Ile Gly Phe						
	260		265		270	
Leu Gly Leu Gly Leu Met Gly Ser Gly Ile Val Ser Asn Leu Leu Lys						
	275		280		285	
Met Gly His Thr Val Thr Val Trp Asn Arg Thr Ala Glu Lys Glu Gly						
	290		295		300	
Ala Arg Leu Gly Arg Thr Pro Ala Glu Val Val Ser Thr Cys Asp Ile						
	305		310		315	320
Thr Phe Ala Cys Val Ser Asp Pro Lys Ala Ala Lys Asp Leu Val Leu						
	325		330		335	
Gly Pro Ser Gly Val Leu Gln Gly Ile Arg Pro Gly Lys Cys Tyr Val						
	340		345		350	
Asp Met Ser Thr Val Asp Ala Asp Thr Val Thr Glu Leu Ala Gln Val						
	355		360		365	
Ile Val Ser Arg Gly Gly Arg Phe Leu Glu Ala Pro Val Ser Gly Asn						
	370		375		380	
Gln Gln Leu Ser Asn Asp Gly Met Leu Val Ile Leu Ala Ala Gly Asp						



385                      390                      395                      400  
 Arg Gly Leu Tyr Glu Asp Cys Ser Ser Cys Phe Gln Ala Met Gly Lys  
                                  405                      410                      415  
 Thr Ser Phe Phe Leu Gly Glu Val Gly Asn Ala Ala Lys Met Met Leu  
                                  420                      425                      430  
 Ile Val Asn Met Val Gln Gly Ser Phe Met Ala Thr Ile Ala Glu Gly  
                                  435                      440                      445  
 Leu Thr Leu Ala Gln Val Thr Gly Gln Ser Gln Gln Thr Leu Leu Asp  
                                  450                      455                      460  
 Ile Leu Asn Gln Gly Gln Leu Ala Ser Ile Phe Leu Asp Gln Lys Cys  
 465                      470                      475                      480  
 Gln Asn Ile Leu Gln Gly Asn Phe Lys Pro Asp Phe Tyr Leu Lys Tyr  
                                  485                      490                      495  
 Ile Gln Lys Asp Leu Arg Leu Ala Ile Ala Leu Gly Asp Ala Val Asn  
                                  500                      505                      510  
 His Pro Thr Pro Met Ala Ala Ala Ala Asn Glu Val Tyr Lys Arg Ala  
                                  515                      520                      525  
 Lys Ala Leu Asp Gln Ser Asp Asn Asp Met Ser Ala Val Tyr Arg Ala  
                                  530                      535                      540  
 Tyr Ile His  
 545

&lt;210&gt; 138

&lt;211&gt; 1097

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 138

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 ggagctggat gatctgatag attctcagaa gaacttagag acttcatcag ccttccagtc 420  
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 caggaatag cccaaatggt ttaaacgcaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1080  
 aaaaaaaaaa aaaaaaa 1097

&lt;210&gt; 139

&lt;211&gt; 232

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 139

Met Leu Gln Glu Tyr Ser Lys Tyr Leu Gln Gln Ala Phe Glu Lys Ser  
 1 5 10 15

Thr Asn Ala Ser Phe Thr Leu Gly His Gly Phe Gln Phe Val Ser Leu  
 20 25 30

Ser Ser Pro Leu His Asn His Thr Leu Phe Pro Glu Lys Gln Ile Tyr  
 35 40 45

Thr Thr Ser Pro Leu Glu Cys Gly Phe Gly Gln Ser Val Thr Ser Val  
 50 55 60

Leu Pro Ser Ser Leu Pro Lys Pro Pro Phe Gly Met Leu Phe Gly Ser  
 65 70 75 80

Gln Pro Gly Leu Tyr Leu Ser Ala Leu Asp Ala Thr His Gln Gln Leu  
 85 90 95

Thr Pro Ser Gln Glu Leu Asp Asp Leu Ile Asp Ser Gln Lys Asn Leu  
 100 105 110

Glu Thr Ser Ser Ala Phe Gln Ser Ser Ser Gln Lys Leu Thr Ser Gln  
 115 120 125

Lys Glu Gln Lys Asn Leu Glu Ser Ser Thr Gly Phe Gln Ile Pro Ser  
 130 135 140

Gln Glu Leu Ala Ser Gln Ile Asp Pro Gln Lys Asp Ile Glu Pro Arg  
 145 150 155 160

Thr Thr Tyr Gln Ile Glu Asn Phe Ala Gln Ala Phe Gly Ser Gln Phe  
 165 170 175

Lys Ser Gly Ser Arg Val Pro Met Thr Phe Ile Thr Asn Ser Asn Gly  
 180 185 190

Glu Val Asp His Arg Val Arg Thr Ser Val Ser Asp Phe Ser Gly Tyr  
 195 200 205

Thr Asn Met Met Ser Asp Val Ser Glu Pro Cys Ser Thr Arg Val Lys  
 210 215 220

Thr Pro Thr Ser Gln Ser Tyr Arg  
 225 230

&lt;210&gt; 140

&lt;211&gt; 775

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 140

gtgtcacata ccactcttgt aggtgtcctc aataatcccc ttttcccaca aaatacacag 60  
 ggtgtattat ctttctcttt attcaccctc actttgctga actgaagta attacatagc 120  
 ctttcttcta acctccttag taatgaacct tcacataaag tgtatttaca gcgtctgtgg 180

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tagccagccc ttctctctct actttcttagg aggggatagc caataactag gaatttaatg 240
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tcctccttaa tcatctgctt acctagtcac tactcaatct gcagaaactt cataaaggaa 360
aagtgtctga ttgtttttac aaataacagt ttgtagggaa aatatgacaa acctcaacta 420
tgggagttgt ccacaatata aaattttgaa aaaacattac atagtataa tatcatactt 480
gggtgttagg cttgttgctt ccccatatca gaggcattca atgatttatc ttttgaatt 540
gctgtgaact tttttaata agccatttag tgtgaaattg tcatgtatca aatgggtatt 600
ggaaatggac tttactcaat ttttaattcca ctgcactcta gccggagtga cagagtaaga 660
ctctgtctca aaaataaata aataaataaa taaataaata aataaataaa taaataaaaa 720
ataataatca aagttttcat aaggaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 775

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&lt;210&gt; 141

&lt;211&gt; 44

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 141

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Met Thr Asn Leu Asn Tyr Gly Ser Cys Pro Gln Tyr Lys Ile Leu Lys
  1             5             10            15

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Lys His Tyr Ile Val Ile Ile Ser Tyr Leu Val Val Arg Leu Val Ala
          20             25             30

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Ser Pro His Gln Arg His Leu Met Ile Tyr Leu Leu
          35             40

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&lt;210&gt; 142

&lt;211&gt; 2060

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 142

```

gaaaaagaag acaaagctca ctttcaggcg gaggtgcagc acctgcgaga ggacaacctg 60
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ttcaacacca tagacatgag ctagggaagg ctgaggagga caggagaagg gccagacac 180
tcctccagtg gagtgcctg cagcccttat tcctccata gaaagcatcc tcagagcacc 240
ttcctgggct tcctactctg cccctttctg gggagtgcac aacacaatag ttgcagatca 300
acaatcatca cctgcctttt gtagaaaaga aaaacaaaaa aagtaataaa aaatttttaa 360
cagtaaaata aaagtttaac tgctaaaatg tgaatgtctt tatttttttg cacaatatct 420
ttatctgtta tgtatttaag aagaaactgg gccttgacc agggcgcccc ctggcccatc 480
cgctcttatt cccatcagct ttcttatcaa cttcaggtaa cccaagcttt cccttggtat 540
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gagggatatt tccttacctt cttccctaaa atgcctggag agggagtgtc tttgagaaaa 660
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```

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tacattgcct gatattctct tgtaaatgag aaatattgct aacatccaag cattctgaag 1860
tcttgcttat ccttctgagt ttagttctca ttttgtttta cattttgttt ggggacttgg 1920
ggcaagctat ttattagagt tttgcaacag agttcttgtt tgaagcctct aaagactacc 1980
tgtaaaattc aaagaataaa attcatttta aacgctcttt taaaaaaaaa aaaaaaaaaa 2040
aaaaaaaaaa aaaaaaaaaa
2060

```

<210> 143  
 <211> 62  
 <212> PRT  
 <213> Homo sapiens

<400> 143  
 Met Thr Val Ile Leu Glu Trp Ala Phe Glu Thr Cys Met Ser Gln Cys  
 1 5 10 15  
 Glu Ile Ser Ala Arg His Phe Leu His Pro Phe Met Ala Ile Gln Arg  
 20 25 30  
 Ile Pro Leu Gln Lys Leu Leu Met Cys Tyr Phe Cys Cys Leu Val Met  
 35 40 45  
 Gln Ala Ala Leu Gly Pro Trp Val Thr Leu Pro Arg Leu Leu  
 50 55 60

<210> 144  
 <211> 1160  
 <212> DNA  
 <213> Homo sapiens

<400> 144  
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 cctcagcctc ccaagtagct gggattacag cctgaaaac cactcgcttg cagagcgctg 180  
 gatcagcaat gcctactagt tcttcattca aacaccggat taaagagcag gaagactaca 240  
 tccgagattg gactgctcat cgagaagaga tagccaggat cagccaagat cttgctctca 300  
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 ccctagtagc cacagtaagc actgctgcca ccacccttg ctctgccata gacactagag 420  
 aagagttggt tgatcggtgt tttgatgaaa gcctcaactt ccaaaagatt cctccattag 480  
 ttcattccaa aacaccagaa ggaaacaacg gtcgatctgg tgatccaaga cctcaagcag 540  
 cagagcctcc cgatcactta acaattacaa ggcggagaac ctggagcagg gatgaagtca 600  
 tgggagataa tctgctgctg tcatccgtct ttcagttctc targaagata agacaatcta 660  
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 ctatgattga tcctgatgga actttggagg ctctgaacaa catgggattt cccagtgtca 900  
 tgttgccatc tccaccgaaa cagaagtcca gccctgtgaa taaccaccac agcccgggtc 960  
 agacaccaac acttggccaa ccagaagcta gggctcttca tctgtgtgct gtttcagccg 1020  
 cagctgaatt tgagaatgct gaatctgagg ctgatttcag tatacatttc aatagagtca 1080  
 accctgatgg ggaagaggaa gatgttacag taacataaat gactttctct tgattgttga 1140  
 aaaaaaaaaa aaaaaaaaaa
 1160

<210> 145  
 <211> 309  
 <212> PRT  
 <213> Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (152)

&lt;400&gt; 145

Met Pro Thr Ser Ser Ser Phe Lys His Arg Ile Lys Glu Gln Glu Asp  
 1 5 10 15

Tyr Ile Arg Asp Trp Thr Ala His Arg Glu Glu Ile Ala Arg Ile Ser  
 20 25 30

Gln Asp Leu Ala Leu Ile Ala Arg Glu Ile Asn Asp Val Ala Gly Glu  
 35 40 45

Ile Asp Ser Val Thr Ser Ser Gly Thr Ala Pro Ser Thr Thr Val Ser  
 50 55 60

Thr Ala Ala Thr Thr Pro Gly Ser Ala Ile Asp Thr Arg Glu Glu Leu  
 65 70 75 80

Val Asp Arg Val Phe Asp Glu Ser Leu Asn Phe Gln Lys Ile Pro Pro  
 85 90 95

Leu Val His Ser Lys Thr Pro Glu Gly Asn Asn Gly Arg Ser Gly Asp  
 100 105 110

Pro Arg Pro Gln Ala Ala Glu Pro Pro Asp His Leu Thr Ile Thr Arg  
 115 120 125

Arg Arg Thr Trp Ser Arg Asp Glu Val Met Gly Asp Asn Leu Leu Leu  
 130 135 140

Ser Ser Val Phe Gln Phe Ser Xaa Lys Ile Arg Gln Ser Ile Asp Lys  
 145 150 155 160

Thr Ala Gly Lys Ile Arg Ile Leu Phe Lys Asp Lys Asp Arg Asn Trp  
 165 170 175

Asp Asp Ile Glu Ser Lys Leu Arg Ala Glu Ser Glu Val Pro Ile Val  
 180 185 190

Lys Thr Ser Ser Met Glu Ile Ser Ser Ile Leu Gln Glu Leu Lys Arg  
 195 200 205

Val Glu Lys Gln Leu Gln Ala Ile Asn Ala Met Ile Asp Pro Asp Gly  
 210 215 220

Thr Leu Glu Ala Leu Asn Asn Met Gly Phe Pro Ser Ala Met Leu Pro  
 225 230 235 240

Ser Pro Pro Lys Gln Lys Ser Ser Pro Val Asn Asn His His Ser Pro  
 245 250 255

Gly Gln Thr Pro Thr Leu Gly Gln Pro Glu Ala Arg Ala Leu His Pro  
 260 265 270

Ala Ala Val Ser Ala Ala Ala Glu Phe Glu Asn Ala Glu Ser Glu Ala  
 275 280 285

Asp Phe Ser Ile His Phe Asn Arg Val Asn Pro Asp Gly Glu Glu Glu

290

295

300

Asp Val Thr Val Thr  
305

<210> 146  
<211> 1536  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> (317)

<400> 146  
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agagaactca cttgtttatt gtggggattt attttctgtc ctcttgcagg gcagaagagg 180  
ggcttaattt cccacatat gatgggaagg accgagtggg aagtctttcc gagaagaact 240  
tcaagcaggt tttaaagaaa tatgacttgc tttgcctcta ctaccatgag cgggtgtctt 300  
cagataaggt cagcnaaaa cagtccaac tgaaagaaat cgtgcttgag cttgtggccc 360  
acgtccttga acataaagct ataggctttg tgatggttga tgccaagaaa gaagccaagc 420  
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caatagagtt tgatggcgag tttgcagctg atgtcttggg ggagtccctc ttggatctaa 540  
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aagactacat caaactcatt ggctttttca agagtgagga ctcaagaatac tacaaggctt 660  
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gaaatgcttg ataccactta gtgtagctcc agcatggatc agcaaacttt ttctgtaaag 1380  
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accagtaaaa gtttatcttag gaaaaaaaaa aaaaaa 1536

<210> 147  
<211> 268  
<212> PRT  
<213> Homo sapiens

<220>  
<221> UNSURE  
<222> (67)

<400> 147  
Met Lys Arg Thr His Leu Phe Ile Val Gly Ile Tyr Phe Leu Ser Ser  
1 5 10 15  
Cys Arg Ala Glu Glu Gly Leu Asn Phe Pro Thr Tyr Asp Gly Lys Asp  
20 25 30  
Arg Val Val Ser Leu Ser Glu Lys Asn Phe Lys Gln Val Leu Lys Lys

35                      40                      45  
 Tyr Asp Leu Leu Cys Leu Tyr Tyr His Glu Pro Val Ser Ser Asp Lys  
     50                      55                      60  
 Val Thr Xaa Lys Gln Phe Gln Leu Lys Glu Ile Val Leu Glu Leu Val  
     65                      70                      75                      80  
 Ala His Val Leu Glu His Lys Ala Ile Gly Phe Val Met Val Asp Ala  
                     85                      90                      95  
 Lys Lys Glu Ala Lys Leu Ala Lys Lys Leu Gly Phe Asp Glu Glu Gly  
                     100                      105                      110  
 Ser Leu Tyr Ile Leu Lys Gly Asp Arg Thr Ile Glu Phe Asp Gly Glu  
                     115                      120                      125  
 Phe Ala Ala Asp Val Leu Val Glu Phe Leu Leu Asp Leu Ile Glu Asp  
                     130                      135                      140  
 Pro Val Glu Ile Ile Ser Ser Lys Leu Glu Val Gln Ala Phe Glu Arg  
                     145                      150                      155                      160  
 Ile Glu Asp Tyr Ile Lys Leu Ile Gly Phe Phe Lys Ser Glu Asp Ser  
                     165                      170                      175  
 Glu Tyr Tyr Lys Ala Phe Glu Glu Ala Ala Glu His Phe Gln Pro Tyr  
                     180                      185                      190  
 Ile Lys Phe Phe Ala Thr Phe Asp Lys Gly Val Ala Lys Lys Leu Ser  
                     195                      200                      205  
 Leu Lys Met Asn Glu Val Asp Phe Tyr Glu Pro Phe Met Asp Glu Pro  
                     210                      215                      220  
 Ile Ala Ile Pro Asn Lys Pro Tyr Thr Glu Glu Glu Leu Val Glu Phe  
                     225                      230                      235                      240  
 Val Lys Glu His Gln Arg Cys Leu Arg Trp His Val Gly Ala Gly Gly  
                     245                      250                      255  
 Leu Gly Ser Gly Glu Trp Arg Gly Ala Ser Leu Cys  
                     260                      265

&lt;210&gt; 148

&lt;211&gt; 1009

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 148

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 aacttgacag gaagtcact tcaagcagat tgacttgaaa cgggatctca ttttaggaagc 120  
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 tgcttatcat tctccttcac tttctgaaaa cctggcaatc ccatgtggac ttctggtaga 240  
 atgagcaatg caaagaactg gcttggactt ggcattgctt tgtacttctg ggggctgatg 300  
 gaccttacga ccaccgttct ctcggacacc ccaacaccac aaggtgaatt agaagcactc 360  
 ctgtcagaca agccacagtc acatcagcgg accaagarga gctggggttg gaaccagttt 420  
 ttcgttcttg aagagtacac tgggaccgac cctttgtatg tcggcaaggt aagaaatgcc 480  
 aagtagaaat gaccgggta gtggatattg aaattgaata tgaattgagt atcaaagttg 540

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gtccatgtct ctggtatgaa tgggaaaaag tgggaattgg gatttggagg aaaaggctca 720
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aaaataaaaa taaaacattt ttcatttcag aagatcttag catgtgcttt aggatagtgt 960
gagacaataa atatatttat aaatgttaaa aaaaaaaaaa aaaaaaaaaa 1009

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&lt;210&gt; 149

&lt;211&gt; 87

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (59)

&lt;400&gt; 149

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Met Trp Thr Ser Gly Arg Met Ser Asn Ala Lys Asn Trp Leu Gly Leu
  1              5              10              15

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Gly Met Ser Leu Tyr Phe Trp Gly Leu Met Asp Leu Thr Thr Thr Val
          20              25              30

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Leu Ser Asp Thr Pro Thr Pro Gln Gly Glu Leu Glu Ala Leu Leu Ser
          35              40              45

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Asp Lys Pro Gln Ser His Gln Arg Thr Lys Xaa Ser Trp Val Trp Asn
          50              55              60

```

```

Gln Phe Phe Val Leu Glu Glu Tyr Thr Gly Thr Asp Pro Leu Tyr Val
          65              70              75              80

```

```

Gly Lys Val Arg Asn Ala Lys
          85

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&lt;210&gt; 150

&lt;211&gt; 2546

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 150

```

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caggaaaaaa ctgaagaggg attaggccct aatataaaaa gcattgtcac catgttgatg 120
ctgatgctat tgatgatgtt tgctgtccac tgtacctggg tcacaagcaa tgcctactct 180
agtccaagtg tagtcctggc ctcatacaat catgatggca ccaggaatat cttagatgat 240
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gcagcctata aaatcatgag gactctagat gtagattatg ttttggttat ttttgaggag 480
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gctgagattg gaaataagga cattaaattc aaacatttgg aagaagcctt tacatcagaa 780
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aaacctcgag tcaccaacat tttcccaaaa cagaagtatt tgtcaaagaa gactacccaa 900
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```

&lt;210&gt; 151

&lt;211&gt; 286

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 151

```

Met Leu Met Leu Met Leu Leu Met Met Phe Ala Val His Cys Thr Trp
  1              5              10              15

```

```

Val Thr Ser Asn Ala Tyr Ser Ser Pro Ser Val Val Leu Ala Ser Tyr
              20              25              30

```

```

Asn His Asp Gly Thr Arg Asn Ile Leu Asp Asp Phe Arg Glu Ala Tyr
              35              40              45

```

```

Phe Trp Leu Arg Gln Asn Thr Asp Glu His Ala Arg Val Met Ser Trp
              50              55              60

```

```

Trp Asp Tyr Gly Tyr Gln Ile Ala Gly Met Ala Asn Arg Thr Thr Leu
              65              70              75              80

```

```

Val Asp Asn Asn Thr Trp Asn Asn Ser His Ile Ala Leu Val Gly Lys
              85              90              95

```

```

Ala Met Ser Ser Asn Glu Thr Ala Ala Tyr Lys Ile Met Arg Thr Leu
              100              105              110

```

```

Asp Val Asp Tyr Val Leu Val Ile Phe Gly Gly Val Ile Gly Tyr Ser
              115              120              125

```

```

Gly Asp Asp Ile Asn Lys Phe Leu Trp Met Val Arg Ile Ala Glu Gly
              130              135              140

```

Glu His Pro Lys Asp Ile Arg Glu Ser Asp Tyr Phe Thr Pro Gln Gly  
145 150 155 160

Glu Phe Arg Val Asp Lys Ala Gly Ser Pro Thr Leu Leu Asn Cys Leu  
165 170 175

Met Tyr Lys Met Ser Tyr Tyr Arg Phe Gly Glu Met Gln Leu Asp Phe  
180 185 190

Arg Thr Pro Pro Gly Phe Asp Arg Thr Arg Asn Ala Glu Ile Gly Asn  
195 200 205

Lys Asp Ile Lys Phe Lys His Leu Glu Glu Ala Phe Thr Ser Glu His  
210 215 220

Trp Leu Val Arg Ile Tyr Lys Val Lys Ala Pro Asp Asn Arg Glu Thr  
225 230 235 240

Leu Asp His Lys Pro Arg Val Thr Asn Ile Phe Pro Lys Gln Lys Tyr  
245 250 255

Leu Ser Lys Lys Thr Thr Lys Arg Lys Arg Gly Tyr Ile Lys Asn Lys  
260 265 270

Leu Val Phe Lys Lys Gly Lys Lys Ile Ser Lys Lys Thr Val  
275 280 285

<210> 152

<211> 4061

<212> DNA

<213> Homo sapiens

<400> 152

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aaraaaaaaa aaaaaaaaaa aaaaaaaaa aaaaaaaaaa a 4061

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&lt;210&gt; 153

&lt;211&gt; 910

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (43)

&lt;400&gt; 153

```

Met Lys Lys Thr Lys Val Arg Leu Met Lys Gln Met Lys Glu Glu Gln
  1             5             10            15

```

```

Glu Lys Ala Arg Leu Thr Glu Ser Arg Arg Asn Arg Glu Ile Ala Gln
          20             25             30

```

Leu Lys Lys Asp Gln Arg Lys Arg Asp His Xaa Leu Arg Leu Leu Glu  
 35 40 45  
 Ala Gln Lys Arg Asn Gln Glu Val Val Leu Arg Arg Lys Thr Glu Glu  
 50 55 60  
 Val Thr Ala Leu Arg Arg Gln Val Arg Pro Met Ser Asp Lys Val Ala  
 65 70 75 80  
 Gly Lys Val Thr Arg Lys Leu Ser Ser Ser Asp Ala Pro Ala Gln Asp  
 85 90 95  
 Thr Gly Ser Ser Ala Ala Ala Val Glu Thr Asp Ala Ser Arg Thr Gly  
 100 105 110  
 Ala Gln Gln Lys Met Arg Ile Pro Val Ala Arg Val Gln Ala Leu Pro  
 115 120 125  
 Thr Pro Ala Thr Asn Gly Asn Arg Lys Lys Tyr Gln Arg Lys Gly Leu  
 130 135 140  
 Thr Gly Arg Val Phe Ile Ser Lys Thr Ala Arg Met Lys Trp Gln Leu  
 145 150 155 160  
 Leu Glu Arg Arg Val Thr Asp Ile Ile Met Gln Lys Met Thr Ile Ser  
 165 170 175  
 Asn Met Glu Ala Asp Met Asn Arg Leu Leu Lys Gln Arg Glu Glu Leu  
 180 185 190  
 Thr Lys Arg Arg Glu Lys Leu Ser Lys Arg Arg Glu Lys Ile Val Lys  
 195 200 205  
 Glu Asn Gly Glu Gly Asp Lys Asn Val Ala Asn Ile Asn Glu Glu Met  
 210 215 220  
 Glu Ser Leu Thr Ala Asn Ile Asp Tyr Ile Asn Asp Ser Ile Ser Asp  
 225 230 235 240  
 Cys Gln Ala Asn Ile Met Gln Met Glu Glu Ala Lys Glu Glu Gly Glu  
 245 250 255  
 Thr Leu Asp Val Thr Ala Val Ile Asn Ala Cys Thr Leu Thr Glu Ala  
 260 265 270  
 Arg Tyr Leu Leu Asp His Phe Leu Ser Met Gly Ile Asn Lys Gly Leu  
 275 280 285  
 Gln Ala Ala Gln Lys Glu Ala Gln Ile Lys Val Leu Glu Gly Arg Leu  
 290 295 300  
 Lys Gln Thr Glu Ile Thr Ser Ala Thr Gln Asn Gln Leu Leu Phe His  
 305 310 315 320  
 Met Leu Lys Glu Lys Ala Glu Leu Asn Pro Glu Leu Asp Ala Leu Leu  
 325 330 335  
 Gly His Ala Leu Gln Asp Leu Asp Ser Val Pro Leu Glu Asn Val Glu  
 340 345 350

Asp Ser Thr Asp Glu Asp Ala Pro Leu Asn Ser Pro Gly Ser Glu Gly  
 355 360 365  
 Ser Thr Leu Ser Ser Asp Leu Met Lys Leu Cys Gly Glu Val Lys Pro  
 370 375 380  
 Lys Asn Lys Ala Arg Arg Arg Thr Thr Thr Gln Met Glu Leu Leu Tyr  
 385 390 395 400  
 Ala Asp Ser Ser Glu Leu Ala Ser Asp Thr Ser Thr Gly Asp Ala Ser  
 405 410 415  
 Leu Pro Gly Pro Leu Thr Pro Val Ala Glu Gly Gln Glu Ile Gly Met  
 420 425 430  
 Asn Thr Glu Thr Ser Gly Thr Ser Ala Arg Glu Lys Glu Leu Ser Pro  
 435 440 445  
 Pro Pro Gly Leu Pro Ser Lys Ile Gly Ser Ile Ser Arg Gln Ser Ser  
 450 455 460  
 Leu Ser Glu Lys Lys Ile Pro Glu Pro Ser Pro Val Thr Arg Arg Lys  
 465 470 475 480  
 Ala Tyr Glu Lys Ala Glu Lys Ser Lys Ala Lys Glu Gln Lys His Ser  
 485 490 495  
 Asp Ser Gly Thr Ser Glu Ala Ser Leu Ser Pro Pro Ser Ser Pro Pro  
 500 505 510  
 Ser Arg Pro Arg Asn Glu Leu Asn Val Phe Asn Arg Leu Thr Val Ser  
 515 520 525  
 Gln Gly Asn Thr Ser Val Gln Gln Asp Lys Ser Asp Glu Ser Asp Ser  
 530 535 540  
 Ser Leu Ser Glu Val His Ser Arg Ser Ser Arg Arg Gly Ile Ile Asn  
 545 550 555 560  
 Pro Phe Pro Ala Ser Lys Gly Ile Arg Ala Phe Pro Leu Gln Cys Ile  
 565 570 575  
 His Ile Ala Glu Gly His Thr Lys Ala Val Leu Cys Val Asp Ser Thr  
 580 585 590  
 Asp Asp Leu Leu Phe Thr Gly Ser Lys Asp Arg Thr Cys Lys Val Trp  
 595 600 605  
 Asn Leu Val Thr Gly Gln Glu Ile Met Ser Leu Gly Gly His Pro Asn  
 610 615 620  
 Asn Val Val Ser Val Lys Tyr Cys Asn Tyr Thr Ser Leu Val Phe Thr  
 625 630 635 640  
 Val Ser Thr Ser Tyr Ile Lys Val Trp Asp Ile Arg Asp Ser Ala Lys  
 645 650 655  
 Cys Ile Arg Thr Leu Thr Ser Ser Gly Gln Val Thr Leu Gly Asp Ala  
 660 665 670

Cys Ser Ala Ser Thr Ser Arg Thr Val Ala Ile Pro Ser Gly Glu Asn  
 675 680 685  
 Gln Ile Asn Gln Ile Ala Leu Asn Pro Thr Gly Thr Phe Leu Tyr Ala  
 690 695 700  
 Ala Ser Gly Asn Ala Val Arg Met Trp Asp Leu Lys Arg Phe Gln Ser  
 705 710 715 720  
 Thr Gly Lys Leu Thr Gly His Leu Gly Pro Val Met Cys Leu Thr Val  
 725 730 735  
 Asp Gln Ile Ser Ser Gly Gln Asp Leu Ile Ile Thr Gly Ser Lys Asp  
 740 745 750  
 His Tyr Ile Lys Met Phe Asp Val Thr Glu Gly Ala Leu Gly Thr Val  
 755 760 765  
 Ser Pro Thr His Asn Phe Glu Pro Pro His Tyr Asp Gly Ile Glu Ala  
 770 775 780  
 Leu Thr Ile Gln Gly Asp Asn Leu Phe Ser Gly Ser Arg Asp Asn Gly  
 785 790 795 800  
 Ile Lys Lys Trp Asp Leu Thr Gln Lys Asp Leu Leu Gln Gln Val Pro  
 805 810 815  
 Asn Ala His Lys Asp Trp Val Cys Ala Leu Gly Val Val Pro Asp His  
 820 825 830  
 Pro Val Leu Leu Ser Gly Cys Arg Gly Gly Ile Leu Lys Val Trp Asn  
 835 840 845  
 Met Asp Thr Phe Met Pro Val Gly Glu Met Lys Gly His Asp Ser Pro  
 850 855 860  
 Ile Asn Ala Ile Cys Val Asn Ser Thr His Ile Phe Thr Ala Ala Asp  
 865 870 875 880  
 Asp Arg Thr Val Arg Ile Trp Lys Ala Arg Asn Leu Gln Asp Gly Gln  
 885 890 895  
 Ile Ser Asp Thr Gly Asp Leu Gly Glu Asp Ile Ala Ser Asn  
 900 905 910

&lt;210&gt; 154

&lt;211&gt; 372

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 154

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 ttggatcagt gctattgtga aaggacttgc accatgaagg gaaccaccta ccgagaattt 180  
 gagtcctgga tagacggctg taagaactgc acatgcctga atggaaccat ccagtgtgaa 240  
 actctaactt gcccaaatcc tgactgccca ctttaagtccg ctcttgcgta tgggatggc 300  
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 gaaagaaata ca 372

<210> 155  
 <211> 761  
 <212> DNA  
 <213> Homo sapiens

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 <222> (108)

<220>  
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 <222> (268)

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 catcagaatt gatgattatt catgtacaga acatgatgag tgtatcaca atcagcacag 420  
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<210> 156  
 <211> 240  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (23)

<220>  
 <221> UNSURE  
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<220>  
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<220>  
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 <222> (87)

<400> 156  
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 35 40 45  
 Arg Asn Xaa Asn Asp Arg Ala Val Cys Ser Cys Arg Asp Gly Phe Arg  
 50 55 60  
 Val Phe Arg Glu Asp Asn Ala Tyr Cys Glu Asp Xaa Asp Glu Cys Ala  
 65 70 75 80  
 Glu Gly Arg His Tyr Cys Xaa Glu Asn Thr Met Cys Val Asn Thr Pro  
 85 90 95  
 Gly Ser Phe Met Cys Ile Cys Lys Thr Gly Tyr Ile Arg Ile Asp Asp  
 100 105 110  
 Tyr Ser Cys Thr Glu His Asp Glu Cys Ile Thr Asn Gln His Ser Cys  
 115 120 125  
 Asp Glu Asn Ala Leu Cys Phe Asn Thr Val Gly Gly His Asn Cys Val  
 130 135 140  
 Cys Lys Pro Gly Tyr Thr Gly Asn Gly Thr Thr Cys Lys Ala Phe Cys  
 145 150 155 160  
 Lys Asp Gly Cys Arg Asn Gly Gly Ala Cys Ile Ala Ala Asn Val Cys  
 165 170 175  
 Ala Cys Pro Gln Gly Phe Thr Gly Pro Ser Cys Glu Thr Asp Ile Asp  
 180 185 190  
 Glu Cys Ser Asp Gly Phe Val Gln Cys Asp Ser Arg Ala Asn Cys Ile  
 195 200 205  
 Asn Leu Pro Gly Trp Tyr His Cys Glu Cys Arg Asp Gly Tyr His Asp  
 210 215 220  
 Asn Gly Met Phe Ser Pro Ser Gly Glu Ser Cys Glu Asp Ile Asp Glu  
 225 230 235 240

&lt;210&gt; 157

&lt;211&gt; 342

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 157

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 atgttatgta cagtacactc tgaaaagaaa tctgaaacaa gttattgtaa tgataaaaaat 180  
 aatgcacagg catggttact taatattttc taacaggaaa agtcatccct atttccttgt 240  
 ttctactgcac ttaattattat ttggttgaat ttgttcagta taagtctcgtt ccttgtgcaa 300  
 aattaaataa atatttttct taccttaaaa aaaaaaaaaa aa 342

&lt;210&gt; 158

&lt;211&gt; 1445

&lt;212&gt; DNA



&lt;213&gt; Homo sapiens

&lt;400&gt; 158

```

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aaaaa 1445

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&lt;210&gt; 159

&lt;211&gt; 245

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 159

```

Met Lys His Thr Gln Ser Gly Gln Ser Thr Ser Pro Leu Val Ile Asp
  1              5              10              15

Tyr Thr Cys Arg Phe Cys Gln Met Ala Phe Val Phe Ser Ser Leu Ile
      20              25              30

Pro Leu Leu Leu Met Thr Pro Val Phe Cys Leu Gly Asn Thr Ser Glu
  35              40              45

Cys Phe Gln Asn Phe Ser Gln Ser His Asn Cys Ile Leu Met His Ser
  50              55              60

Pro Pro Ser Ala Met Ala Glu Leu Pro Pro Ser Ala Asn Thr Ser Val
  65              70              75              80

Cys Ser Thr Leu Tyr Phe Tyr Gly Ile Ala Ile Phe Leu Gly Ser Phe
      85              90              95

Val Leu Ser Leu Leu Thr Ile Met Val Leu Leu Ile Arg Ala Gln Thr
  100              105              110

Leu Tyr Lys Lys Phe Val Lys Ser Thr Gly Phe Leu Gly Ser Glu Gln
  115              120              125

Trp Ala Val Ile His Ile Val Asp Gln Arg Val Arg Phe Tyr Pro Val

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130                      135                      140  
 Ala Phe Phe Cys Cys Trp Gly Pro Ala Val Ile Leu Met Ile Ile Lys  
 145                      150                      155                      160  
 Leu Thr Lys Pro Gln Asp Thr Lys Leu His Met Ala Leu Tyr Val Leu  
                     165                      170                      175  
 Gln Ala Leu Thr Ala Thr Ser Gln Gly Leu Leu Asn Cys Gly Val Tyr  
                     180                      185                      190  
 Gly Trp Thr Gln His Lys Phe His Gln Leu Lys Gln Glu Ala Arg Arg  
                     195                      200                      205  
 Asp Ala Asp Thr Gln Thr Pro Leu Leu Cys Ser Gln Lys Arg Phe Tyr  
                     210                      215                      220  
 Ser Arg Gly Leu Asn Ser Leu Glu Ser Thr Leu Thr Phe Pro Ala Ser  
 225                      230                      235                      240  
 Thr Ser Thr Ile Phe  
                     245

&lt;210&gt; 160

&lt;211&gt; 3550

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 160

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aaaaaaaaa 3550

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<210> 161  
 <211> 975  
 <212> PRT  
 <213> Homo sapiens

<400> 161

Met Arg Ser Glu Ala Leu Leu Leu Tyr Phe Thr Leu Leu His Phe Ala  
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Gly Ala Gly Phe Pro Glu Asp Ser Glu Pro Ile Ser Ile Ser His Gly  
                   20                  25                  30

Asn Tyr Thr Lys Gln Tyr Pro Val Phe Val Gly His Lys Pro Gly Arg  
           35                  40                  45

Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met  
           50                  55                  60

Asn Gly Thr Leu Tyr Ile Ala Ala Arg Asp His Ile Tyr Thr Val Asp  
           65                  70                  75                  80

Ile Asp Thr Ser His Thr Glu Glu Ile Tyr Cys Ser Lys Lys Leu Thr  
                   85                  90                  95

Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys  
           100                  105                  110

His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn  
           115                  120                  125

Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys  
 130 135 140  
 Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser  
 145 150 155 160  
 Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu  
 165 170 175  
 Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala  
 180 185 190  
 Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg  
 195 200 205  
 Thr Val Lys His Asp Ser Lys Trp Leu Lys Glu Pro Tyr Phe Val Gln  
 210 215 220  
 Ala Val Asp Tyr Gly Asp Tyr Ile Tyr Phe Phe Phe Arg Glu Ile Ala  
 225 230 235 240  
 Val Glu Tyr Asn Thr Met Gly Lys Val Val Phe Pro Arg Val Ala Gln  
 245 250 255  
 Val Cys Lys Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys Gln  
 260 265 270  
 Trp Thr Ser Phe Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp  
 275 280 285  
 Ser His Phe Tyr Phe Asn Ile Leu Gln Ala Val Thr Asp Val Ile Arg  
 290 295 300  
 Ile Asn Gly Arg Asp Val Val Leu Ala Thr Phe Ser Thr Pro Tyr Asn  
 305 310 315 320  
 Ser Ile Pro Gly Ser Ala Val Cys Ala Tyr Asp Met Leu Asp Ile Ala  
 325 330 335  
 Ser Val Phe Thr Gly Arg Phe Lys Glu Gln Lys Ser Pro Asp Ser Thr  
 340 345 350  
 Trp Thr Pro Val Pro Asp Glu Arg Val Pro Lys Pro Arg Pro Gly Cys  
 355 360 365  
 Cys Ala Gly Ser Ser Ser Leu Glu Arg Tyr Ala Thr Ser Asn Glu Phe  
 370 375 380  
 Pro Asp Asp Thr Leu Asn Phe Ile Lys Thr His Pro Leu Met Asp Glu  
 385 390 395 400  
 Ala Val Pro Ser Ile Phe Asn Arg Pro Trp Phe Leu Arg Thr Met Val  
 405 410 415  
 Arg Tyr Arg Leu Thr Lys Ile Ala Val Asp Thr Ala Ala Gly Pro Tyr  
 420 425 430  
 Gln Asn His Thr Val Val Phe Leu Gly Ser Glu Lys Gly Ile Ile Leu  
 435 440 445

Lys Phe Leu Ala Arg Ile Gly Asn Ser Gly Phe Leu Asn Asp Ser Leu  
 450 455 460  
 Phe Leu Glu Glu Met Ser Val Tyr Asn Ser Glu Lys Cys Ser Tyr Asp  
 465 470 475 480  
 Gly Val Glu Asp Lys Arg Ile Met Gly Met Gln Leu Asp Arg Ala Ser  
 485 490 495  
 Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu  
 500 505 510  
 Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser  
 515 520 525  
 Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His  
 530 535 540  
 Leu Ser Pro Asn Ser Arg Leu Thr Phe Glu Gln Asp Ile Glu Arg Gly  
 545 550 555 560  
 Asn Thr Asp Gly Leu Gly Asp Cys His Asn Ser Phe Val Ala Leu Asn  
 565 570 575  
 Gly Val Ile Arg Glu Ser Tyr Leu Lys Gly His Asp Gln Leu Val Pro  
 580 585 590  
 Val Thr Leu Leu Ala Ile Ala Val Ile Leu Ala Phe Val Met Gly Ala  
 595 600 605  
 Val Phe Ser Gly Ile Thr Val Tyr Cys Val Cys Asp His Arg Arg Lys  
 610 615 620  
 Asp Val Ala Val Val Gln Arg Lys Glu Lys Glu Leu Thr His Ser Arg  
 625 630 635 640  
 Arg Gly Ser Met Ser Ser Val Thr Lys Leu Ser Gly Leu Phe Gly Asp  
 645 650 655  
 Thr Gln Ser Lys Asp Pro Lys Pro Glu Ala Ile Leu Thr Pro Leu Met  
 660 665 670  
 His Asn Gly Lys Leu Ala Thr Pro Gly Asn Thr Ala Lys Met Leu Ile  
 675 680 685  
 Lys Ala Asp Gln His His Leu Asp Leu Thr Ala Leu Pro Thr Pro Glu  
 690 695 700  
 Ser Thr Pro Thr Leu Gln Gln Lys Arg Lys Pro Ser Arg Gly Ser Arg  
 705 710 715 720  
 Glu Trp Glu Arg Asn Gln Asn Leu Ile Asn Ala Cys Thr Lys Asp Met  
 725 730 735  
 Pro Pro Met Gly Ser Pro Val Ile Pro Thr Asp Leu Pro Leu Arg Ala  
 740 745 750  
 Ser Pro Ser His Ile Pro Ser Val Val Val Leu Pro Ile Thr Gln Gln  
 755 760 765

Gly Tyr Gln His Glu Tyr Val Asp Gln Pro Lys Met Ser Glu Val Ala  
 770 775 780  
 Gln Met Ala Leu Glu Asp Gln Ala Ala Thr Leu Glu Tyr Lys Thr Ile  
 785 790 795 800  
 Lys Glu His Phe Ser Ser Lys Ser Pro Asn His Gly Val Asn Leu Val  
 805 810 815  
 Glu Asn Leu Asp Ser Leu Pro Pro Lys Val Pro Gln Arg Glu Ala Ser  
 820 825 830  
 Leu Gly Pro Pro Gly Ala Ser Leu Phe Gln Thr Gly Leu Ser Lys Arg  
 835 840 845  
 Leu Glu Met His His Ser Phe Ser Tyr Gly Val Asp Tyr Lys Arg Ser  
 850 855 860  
 Tyr Pro Thr Asn Ser Leu Thr Arg Ser His Gln Ala Thr Thr Leu Lys  
 865 870 875 880  
 Arg Asn Asn Thr Asn Ser Ser Asn Ser Ser His Leu Ser Arg Asn Gln  
 885 890 895  
 Ser Phe Gly Arg Gly Asp Asn Pro Pro Pro Ala Pro Gln Arg Val Asp  
 900 905 910  
 Ser Ile Gln Val His Ser Ser Gln Pro Ser Gly Gln Ala Val Thr Val  
 915 920 925  
 Ser Arg Gln Pro Ser Leu Asn Ala Tyr Asn Ser Leu Thr Arg Ser Gly  
 930 935 940  
 Leu Lys Arg Thr Pro Ser Leu Lys Pro Asp Val Pro Pro Lys Pro Ser  
 945 950 955 960  
 Phe Ala Pro Leu Ser Thr Ser Met Lys Pro Asn Asp Ala Cys Thr  
 965 970 975

&lt;210&gt; 162

&lt;211&gt; 1723

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 162

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 actggagcag taggaggtgt ggggtcattt tatgaatata ataaaatgga gctgactatg 180  
 gacrrrgact wagtgtgggg gagaggggac gatacagggt gtgtgtcttg gagtgccttg 240  
 gggacagggg ccccccggtg gtcctatggc aggatgagaa rggagggact tggctcccc 300  
 agagcccggt ggaagctact gttctctcca gtgtctcgag cgtagccaaa ataagggttg 360  
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 cactgtagtc caggtcgtg gtggcagcgg gggcaagggg aggggcaagg ctgccccac 540  
 cccacgcacc aagtcacgcc aagtctcagc aggtaaaagc acgtgagcct agggcgagcg 600  
 gagggagtcc tgggtggcccc gcaggtcagg agggaaagca gggctcagag ggcacgttg 660  
 ccccagggca gggctctacc tgggggtcag gagcaccttg gtcttgatga ttgattgatt 720  
 gatagaatgg agctgggtct gagcctccca ggcttgagct cctgggagtt ctgtgctggt 780

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&lt;210&gt; 163

&lt;211&gt; 101

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (49)

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (51)

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (81)

&lt;400&gt; 163

```

Val Phe Arg Cys Pro Leu Leu Ile Gly Tyr Ile Asn Leu Leu Thr Leu
  1             5             10             15

```

```

Gly Val Thr Val Leu Ala Thr Phe Arg Gly Val Thr Gly Ala Val Gly
      20             25             30

```

```

Gly Val Gly Ser Phe Tyr Glu Tyr Asn Lys Met Glu Leu Thr Met Asp
  35             40             45

```

```

Xaa Asp Xaa Val Trp Gly Arg Gly Asp Asp Thr Gly Cys Val Ser Gly
  50             55             60

```

```

Ser Ala Trp Gly Thr Gly Thr Pro Arg Trp Ser Tyr Gly Arg Met Arg
  65             70             75             80

```

```

Xaa Glu Gly Leu Gly Ser Pro Arg Ala Arg Trp Lys Leu Leu Phe Ser
      85             90             95

```

```

Pro Val Ser Arg Ala
      100

```

&lt;210&gt; 164

&lt;211&gt; 469

&lt;212&gt; DNA

<213> Homo sapiens

<400> 164

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tcgccccctc aaatcacctc ctcccgtagc ccaccgact aacatctcag tctctgaaaa 180
tgcacagaga tgcctggcta cctcgccctg ccttcagcct cacggggctc agtctctttt 240
tctcttttgt gccaccagga cggagcatgg aggtcacagt acctgccacc ctcaacgtcc 300
tcaatggctc tgacgccgc ctgccctgca ccttcaactc ctgctacaca gtgaaccaca 360
aacagtcttc cctgaactgg acttaccagg agtgcaacaa ctgctctgag gagatgttcc 420
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<210> 165

<211> 96

<212> PRT

<213> Homo sapiens

<400> 165

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Met His Arg Asp Ala Trp Leu Pro Arg Pro Ala Phe Ser Leu Thr Gly
 1             5             10             15

Leu Ser Leu Phe Phe Ser Leu Val Pro Pro Gly Arg Ser Met Glu Val
          20             25             30

Thr Val Pro Ala Thr Leu Asn Val Leu Asn Gly Ser Asp Ala Arg Leu
      35             40             45

Pro Cys Thr Phe Asn Ser Cys Tyr Thr Val Asn His Lys Gln Phe Ser
      50             55             60

Leu Asn Trp Thr Tyr Gln Glu Cys Asn Asn Cys Ser Glu Glu Met Phe
 65             70             75             80

Leu Gln Phe Arg Met Lys Ile Ile Asn Leu Lys Leu Glu Arg Phe Gln
          85             90             95

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<210> 166

<211> 454

<212> DNA

<213> Homo sapiens

<400> 166

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aacaactcct ttggtgggga caaaagtgac aattgtaggc caggcacagt ggctcacgcc 180
tgtaatccca gcacttttgg aggccaaggc ggttgattta cctccatctg tttagtagaa 240
atggggcaaaa ccccatTTTT actaaaaata caagaattag ctgggcgtgg tggcgtgtgc 300
ctgtaatccc agctatttgg gaggctgagg caggagaatc gcttgagccc gggaagcaga 360
ggttgcaagt aactgagata gtgatagtgc cactgcaatt cagcctgggt gacatagaga 420
gactccatct caaaaaaaaaa aaaaaaaaaa aaaa 454

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<210> 167

<211> 736

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (680)



<220>  
 <221> unsure  
 <222> (704)

<400> 167  
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 ttgcagcaaa ctaataacac ctggatttct caatttatta agttgtactt acctgatgct 180  
 gatgatgatt actgtattta cacattgtct cagagctcac tcttgcgag gttgtggcct 240  
 cgaaaatgcc ttgttgcccc tctggaatct gtcttttcag cttcatctcc tcctcctcac 300  
 ctccctgtgt ggtgcacaga tacctatagg caggctccat ctccctctcc ccagctcttc 360  
 ccctagtgcg cagataccta taggcaggct tcctctcttc ctccccagct tctcccctag 420  
 tgcacagata cctataggca ggctccatct cctcctcccc agctcctccc ctartgcaca 480  
 gacacctata ggcaagctcc atctcctcct ctttagctag cctccccatc tcatcacaaac 540  
 gcatgtctgt gaccttttgt aatcatttac agtgccacac ggaaccctgt attttgcaca 600  
 cagcaaaaaca aacaatgttt agcttttatt atggtatttg atgactgtaa atggaaataa 660  
 atattgttct ttattttttt aaaaaaaaaa aaaaaaaaaa aaanaaaaaa aaaaaaaaaa 720  
 aaaaaaaaaa aaaaaa 736

<210> 168  
 <211> 114  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (100)

<400> 168  
 Met Leu Met Met Ile Thr Val Phe Thr His Cys Leu Arg Ala His Ser  
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 Cys Gly Gly Cys Gly Leu Glu Asn Ala Leu Leu Ser Leu Trp Asn Leu  
 20 25 30  
 Ser Phe Gln Leu His Leu Leu Leu Thr Ser Cys Cys Gly Ala Gln  
 35 40 45  
 Ile Pro Ile Gly Arg Leu His Leu Leu Leu Pro Ser Ser Ser Pro Ser  
 50 55 60  
 Ala Gln Ile Pro Ile Gly Arg Leu His Leu Leu Leu Pro Ser Phe Ser  
 65 70 75 80  
 Pro Ser Ala Gln Ile Pro Ile Gly Arg Leu His Leu Leu Leu Pro Ser  
 85 90 95  
 Ser Ser Pro Xaa Ala Gln Thr Pro Ile Gly Lys Leu His Leu Leu Leu  
 100 105 110  
 Phe Ser

<210> 169  
 <211> 1427  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 169

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tgatcagttg tttaatggga gatctgaaat gttaaactca gaccagaaaag aagagaacct 180
gttttctaga aattaggttt ttaatccaag taagatgcaa gcttttgctt ttttaataac 240
ttgtatagct aaaaacttga cggtgaaaag ctctcagatc aaagctgac cttctgtcag 300
taatgattct aaaaataagc aagattttta tggggaatat attttatttc attcttatct 360
caaacctagg tactgtggtc gttttgagtt catttcgagg cattttcaat gtgcctcagg 420
ccacatccaa cctctyccca gggccagatt taatgttcag cctcataaag gttatcatag 480
ttttaacatt taagtactat tttgcagtgg gtatatacca aaatttgcta atagtaagat 540
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caagaaattc atgttctatc ttggaggcaa taaacaaaca tttttgttc aaaattaggg 660
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gtatagatgt accacagttt gtttaactgt tcacctgctg agagacattg ggccagtttt 1380
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&lt;210&gt; 170

&lt;211&gt; 79

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (45)

&lt;400&gt; 170

```

Met Ile Leu Lys Ile Ser Lys Ile Leu Met Gly Asn Ile Phe Tyr Phe
 1             5             10            15

Ile Leu Ile Ser Asn Leu Gly Thr Val Val Val Leu Ser Ser Phe Arg
 20             25            30

Gly Ile Phe Asn Val Pro Gln Ala Thr Ser Asn Leu Xaa Pro Gly Pro
 35             40            45

Asp Leu Met Phe Ser Leu Ile Lys Val Ile Ile Val Leu Thr Phe Lys
 50             55            60

Tyr Tyr Phe Ala Val Gly Ile Tyr Gln Asn Leu Leu Ile Val Arg
 65             70            75

```

&lt;210&gt; 171

&lt;211&gt; 572

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 171

```

tgcagattct gtggttatac tcactcctca tcccaaagaa tgaaatttac cactctctc 60
ttcttggcag ctgtagcagg ggccctggtc tatgctgaag atgcctctc tgactcgacg 120

```

ggtgctgac ctgcccagga agctgggacc tctaagccta atgaagagat ctcagggtcca 180  
 gcagaaccag cttcaccccc agagacaacc acaacagccc aggagacttc ggcggcagca 240  
 gttcagggga cagccaaggt cacctcaagc aggcaggaac taaacccccct gaaatccata 300  
 gtggagaaaa gtatcttact aacagaacaa gcccttgcaa aagcaggaaa aggaatgcac 360  
 ggaggcgtgc cagggtggaaa acaattcatc gaaaatggaa gtgaatttgc acaaaaatta 420  
 ctgaagaaat tcagtctatt aaaaccatgg gcatgagaag ctgaaaagaa tgggatcatt 480  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 572

<210> 172

<211> 138

<212> PRT

<213> Homo sapiens

<400> 172

Met Lys Phe Thr Thr Leu Leu Phe Leu Ala Ala Val Ala Gly Ala Leu  
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Val Tyr Ala Glu Asp Ala Ser Ser Asp Ser Thr Gly Ala Asp Pro Ala  
 20 25 30

Gln Glu Ala Gly Thr Ser Lys Pro Asn Glu Glu Ile Ser Gly Pro Ala  
 35 40 45

Glu Pro Ala Ser Pro Pro Glu Thr Thr Thr Thr Ala Gln Glu Thr Ser  
 50 55 60

Ala Ala Ala Val Gln Gly Thr Ala Lys Val Thr Ser Ser Arg Gln Glu  
 65 70 75 80

Leu Asn Pro Leu Lys Ser Ile Val Glu Lys Ser Ile Leu Leu Thr Glu  
 85 90 95

Gln Ala Leu Ala Lys Ala Gly Lys Gly Met His Gly Gly Val Pro Gly  
 100 105 110

Gly Lys Gln Phe Ile Glu Asn Gly Ser Glu Phe Ala Gln Lys Leu Leu  
 115 120 125

Lys Lys Phe Ser Leu Leu Lys Pro Trp Ala  
 130 135

<210> 173

<211> 1223

<212> DNA

<213> Homo sapiens

<400> 173

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 ttggcactac cggcagtcct gttcagaatg agcaaggcct tgtggagttc aaaatttctg 180  
 ggccctctgca gtacatgtgg tggtagcatg tgggtggcct gatttggatc agtgaattta 240  
 ttctagcatg tcagcagatg acagtggcag gagctgtggt aacatactat ttactagggt 300  
 ataaaaggaa tttgccattt acacctattt tggcatcagt aaatcgctt atycgttacc 360  
 acctaggtac ggtggcaaaa ggatctttca ttatcacatt agtcaaaatt ccgcgaatga 420  
 tccttatgta tattcacagt cagctcaaag gaaaggaaaa tgcttggtgca cgatgtgtgc 480  
 tgaaatcttg catttggtgc ctttggtgtc ttgaaaagtg cctaaattat ttaaatcaga 540  
 atgcatacac agccacagct atcaacagca ccaacttctg cacctcagca aaggatgcct 600  
 ttgtcattct ggtggagaat gctttgcgag tggctaccat caacacagta ggagatttta 660

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ctttcctagt cgctcattgc ttctgtctta tttatgaaat ggtagtggat gtattattct 840
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caaaagcaaa aaaaaaaaaa aaa 1223

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<210> 174  
 <211> 301  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (246)..(247)

<220>  
 <221> UNSURE  
 <222> (251)

<220>  
 <221> UNSURE  
 <222> (258)

<400> 174  
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 Gln Gly Phe Val Glu Phe Lys Ile Ser Gly Pro Leu Gln Tyr Met Trp  
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 Trp Tyr His Val Val Gly Leu Ile Trp Ile Ser Glu Phe Ile Leu Ala  
 35 40 45  
 Cys Gln Gln Met Thr Val Ala Gly Ala Val Val Thr Tyr Tyr Phe Thr  
 50 55 60  
 Arg Asp Lys Arg Asn Leu Pro Phe Thr Pro Ile Leu Ala Ser Val Asn  
 65 70 75 80  
 Arg Leu Ile Arg Tyr His Leu Gly Thr Val Ala Lys Gly Ser Phe Ile  
 85 90 95  
 Ile Thr Leu Val Lys Ile Pro Arg Met Ile Leu Met Tyr Ile His Ser  
 100 105 110  
 Gln Leu Lys Gly Lys Glu Asn Ala Cys Ala Arg Cys Val Leu Lys Ser  
 115 120 125  
 Cys Ile Cys Cys Leu Trp Cys Leu Glu Lys Cys Leu Asn Tyr Leu Asn  
 130 135 140  
 Gln Asn Ala Tyr Thr Ala Thr Ala Ile Asn Ser Thr Asn Phe Cys Thr  
 145 150 155 160  
 Ser Ala Lys Asp Ala Phe Val Ile Leu Val Glu Asn Ala Leu Arg Val

165 170 175

Ala Thr Ile Asn Thr Val Gly Asp Phe Met Leu Phe Leu Gly Lys Val  
180 185 190

Leu Ile Val Cys Ser Thr Gly Leu Ala Gly Ile Met Leu Leu Asn Tyr  
195 200 205

Gln Gln Asp Tyr Thr Val Trp Val Leu Pro Leu Ile Ile Val Cys Leu  
210 215 220

Phe Ala Phe Leu Val Ala His Cys Phe Leu Ser Ile Tyr Glu Met Val  
225 230 235 240

Val Asp Val Leu Phe Xaa Xaa Phe Ala Ile Xaa Thr Lys Tyr Asn Asp  
245 250 255

Gly Xaa Pro Gly Arg Glu Phe Tyr Met Asp Lys Val Leu Met Glu Phe  
260 265 270

Val Glu Asn Ser Arg Lys Ala Met Lys Glu Ala Gly Lys Gly Gly Val  
275 280 285

Ala Asp Ser Arg Glu Leu Lys Pro Met Leu Lys Lys Arg  
290 295 300

&lt;210&gt; 175

&lt;211&gt; 2460

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 175

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tctcactca gcatcgaggg agactaacia actccgggca aagttggggc tgaaccctt 120  
ggagggttaat gccatcaaga aggagggcggg caccaaggag gagcccgta cagctgatgt 180  
catcaaccct atggccttgc gacagcgaga ggagctgcgg gagaagctgg cggctgccaa 240  
ggagaagcgc ctgctgaacc aaaagctggg gaagataaag accctaggag aggatgaccc 300  
ctggctggac gacactgcag cctggatcga gaggagccgg cagctgcaga aggagaagga 360  
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```

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```

&lt;210&gt; 176

&lt;211&gt; 563

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 176

```

Met Thr Ala Thr Arg Pro Leu Pro Ala Pro Lys Leu Ala Gln Ala Met
  1                      5                      10                      15

```

```

Pro Pro His Ser Ala Ser Arg Glu Thr Asn Lys Leu Arg Ala Lys Leu
          20                      25                      30

```

```

Gly Leu Lys Pro Leu Glu Val Asn Ala Ile Lys Lys Glu Ala Gly Thr
      35                      40                      45

```

```

Lys Glu Glu Pro Val Thr Ala Asp Val Ile Asn Pro Met Ala Leu Arg
      50                      55                      60

```

```

Gln Arg Glu Glu Leu Arg Glu Lys Leu Ala Ala Ala Lys Glu Lys Arg
      65                      70                      75                      80

```

```

Leu Leu Asn Gln Lys Leu Gly Lys Ile Lys Thr Leu Gly Glu Asp Asp
          85                      90                      95

```

```

Pro Trp Leu Asp Asp Thr Ala Ala Trp Ile Glu Arg Ser Arg Gln Leu
      100                      105                      110

```

```

Gln Lys Glu Lys Asp Leu Ala Glu Lys Arg Ala Lys Leu Leu Glu Glu
      115                      120                      125

```

```

Met Asp Gln Lys Phe Gly Val Ser Thr Leu Val Glu Glu Glu Phe Gly
      130                      135                      140

```

```

Gln Arg Arg Gln Asp Leu Tyr Ser Ala Arg Asp Leu Gln Gly Leu Thr
      145                      150                      155                      160

```

```

Val Glu His Ala Ile Asp Ser Phe Arg Glu Gly Glu Thr Met Ile Leu
          165                      170                      175

```

```

Thr Leu Lys Asp Lys Gly Val Leu Gln Glu Glu Glu Asp Val Leu Val
      180                      185                      190

```

```

Asn Val Asn Leu Val Asp Lys Glu Arg Ala Glu Lys Asn Val Glu Leu
      195                      200                      205

```

Arg Lys Lys Lys Pro Asp Tyr Leu Pro Tyr Ala Glu Asp Glu Ser Val  
 210 215 220  
 Asp Asp Leu Ala Gln Gln Lys Pro Arg Ser Ile Leu Ser Lys Tyr Asp  
 225 230 235 240  
 Glu Lys Leu Glu Gly Glu Arg Pro His Ser Phe Arg Leu Glu Gln Gly  
 245 250 255  
 Gly Thr Ala Asp Gly Leu Arg Glu Arg Glu Leu Glu Glu Ile Arg Ala  
 260 265 270  
 Lys Leu Arg Leu Gln Ala Gln Ser Leu Ser Thr Val Gly Pro Arg Leu  
 275 280 285  
 Ala Ser Glu Tyr Leu Thr Pro Glu Glu Met Val Thr Phe Lys Lys Thr  
 290 295 300  
 Lys Arg Arg Val Lys Lys Ile Arg Lys Lys Glu Lys Glu Val Val Val  
 305 310 315 320  
 Arg Ala Asp Asp Leu Leu Pro Leu Gly Asp Gln Thr Gln Asp Gly Asp  
 325 330 335  
 Phe Gly Ser Arg Leu Arg Gly Arg Gly Arg Arg Arg Val Ser Glu Val  
 340 345 350  
 Glu Glu Glu Lys Glu Pro Val Pro Gln Pro Leu Pro Ser Asp Asp Thr  
 355 360 365  
 Arg Val Glu Asn Met Asp Ile Ser Asp Glu Glu Glu Gly Gly Ala Pro  
 370 375 380  
 Pro Pro Gly Ser Pro Gln Val Leu Glu Glu Asp Glu Ala Glu Leu Glu  
 385 390 395 400  
 Leu Gln Lys Gln Leu Glu Lys Gly Arg Arg Leu Arg Gln Leu Gln Gln  
 405 410 415  
 Leu Gln Gln Leu Arg Asp Ser Gly Glu Lys Val Val Glu Ile Val Lys  
 420 425 430  
 Lys Leu Glu Ser Arg Gln Arg Gly Trp Glu Glu Asp Glu Asp Pro Glu  
 435 440 445  
 Arg Lys Gly Ala Ile Val Phe Asn Ala Thr Ser Glu Phe Cys Arg Thr  
 450 455 460  
 Leu Gly Glu Ile Pro Thr Tyr Gly Leu Ala Gly Asn Arg Glu Glu Gln  
 465 470 475 480  
 Glu Glu Leu Met Asp Phe Glu Arg Asp Glu Glu Arg Ser Ala Asn Gly  
 485 490 495  
 Gly Ser Glu Ser Asp Gly Glu Glu Asn Ile Gly Trp Ser Thr Val Asn  
 500 505 510  
 Leu Asp Glu Glu Lys Gln Gln Gln Asp Val Arg Ala Thr Pro Leu Gly  
 515 520 525

Gly Gly Arg Leu Gly Val Leu Lys Leu Glu Met Ser Thr Gly Leu Gly  
530 535 540

Val Gln Ser Leu Ser Leu Leu Ile Gln Ser Gly Leu Cys Arg Pro Pro  
545 550 555 560

Arg Ala Ile

<210> 177  
<211> 1790  
<212> DNA  
<213> Homo sapiens

<400> 177  
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cagtttggtg acctagtga ttgattcttt ccattttcta tactattcac cagcatatca 540  
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ttctctcttg cactgttttg tacattacag ccaccattag ccttaaaagc tgcagcagcc 1740  
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<210> 178  
<211> 115  
<212> PRT  
<213> Homo sapiens

<400> 178  
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20 25 30  
Thr Ile Asn Leu Ser Asn Ser Ala Glu Ser Leu Gln Phe Thr Ala Leu



35

40

45

Asn Pro Ser Leu Gln Thr Lys Ala Asn Leu Met Ser Ser Asn Ser Tyr  
50 55 60

Asn Ser Leu Leu Ser Gln Phe Arg Leu Gln Arg Leu His Leu Arg Gly  
65 70 75 80

Asn Leu Lys Asn Lys Gln Cys Ser Ile Ser Val His Ile Lys Gly Thr  
85 90 95

Ser Asn Arg Asn Leu Ser Leu Leu Leu Ser Leu Cys Tyr Trp Thr Leu  
100 105 110

Ser Ser Arg  
115

<210> 179

<211> 2026

<212> DNA

<213> Homo sapiens

<400> 179

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agtttgcacc ctttttgtat gtaaaataaa atgtcttacc ttcttgggt aaaaaaaaaa 1980  
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2026

<210> 180

<211> 52  
 <212> PRT  
 <213> Homo sapiens

<400> 180

Met Leu Gln Arg Asn Leu Arg Ser Val Asp Arg Ile Ser Phe Ile Phe  
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Leu Leu Leu Leu Leu Thr Ile Thr Phe Pro Val Pro Ser Pro Ser Ile  
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Arg Ser Gln Ser Arg Gly Leu Phe Met Val Ile Ser Gly Gly Val Val  
 35 40 45

Gln Pro Phe Gln  
 50

<210> 181  
 <211> 1138  
 <212> DNA  
 <213> Homo sapiens

<400> 181

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 gatgacattg atcttgatgc cttggctgca gaaatagaag gagctggtgc tgccaaagaa 240  
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<210> 182  
 <211> 209  
 <212> PRT  
 <213> Homo sapiens

<400> 182

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 20 25 30

Lys Glu Gln Glu Prc Gln Lys Ser Lys Gly Lys Lys Lys Lys Glu Lys  
 35 40 45

Lys Lys Gln Asp Phe Asp Glu Asp Asp Ile Leu Lys Glu Leu Glu Glu

50                      55                      60  
 Leu Ser Leu Glu Ala Gln Gly Ile Lys Ala Asp Arg Glu Thr Val Ala  
 65                      70                      75                      80  
 Val Lys Pro Thr Glu Asn Asn Glu Glu Glu Phe Thr Ser Lys Asp Lys  
                     85                      90                      95  
 Lys Lys Lys Gly Gln Lys Gly Lys Lys Gln Ser Phe Asp Asp Asn Asp  
                     100                      105                      110  
 Ser Glu Glu Leu Glu Asp Lys Asp Ser Lys Ser Lys Lys Thr Ala Lys  
                     115                      120                      125  
 Pro Lys Val Glu Met Tyr Ser Gly Ser Asp Asp Asp Asp Asp Phe Asn  
                     130                      135                      140  
 Lys Leu Pro Lys Lys Ala Lys Gly Lys Ala Gln Lys Ser Asn Lys Lys  
 145                      150                      155                      160  
 Trp Asp Gly Ser Glu Glu Asp Glu Asp Asn Ser Lys Lys Ile Lys Glu  
                     165                      170                      175  
 Arg Ser Arg Ile Asn Ser Ser Gly Glu Ser Gly Asp Glu Ser Asp Glu  
                     180                      185                      190  
 Phe Leu Gln Ser Lys Arg Thr Glu Lys Lys Ser Glu Lys Gln Ala Arg  
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Ser

<210> 183

<211> 912

<212> DNA

<213> Homo sapiens

<400> 183

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 cctgtgaagg agagcttcaa gttggcaaag gagatgaagt cacaattaca ctgccacata 240  
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 aacacctca gaaatgactt gcagttgagt gagtytgga gtgacagtga tgactagtgc 720  
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<210> 184

<211> 167

<212> PRT

<213> Homo sapiens

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<220>  
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<400> 184

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Lys Ile Gln Ala Arg Met Glu Gln Gln Pro Thr Arg Pro Pro Gln Thr  
 20 25 30

Ser Gln Pro Pro Pro Pro Pro Pro Met Pro Phe Arg Ala Pro Thr  
 35 40 45

Lys Pro Pro Val Gly Pro Lys Thr Ser Pro Leu Lys Asp Asn Pro Ser  
 50 55 60

Pro Glu Pro Gln Leu Asp Asp Ile Lys Arg Glu Leu Arg Ala Glu Val  
 65 70 75 80

Asp Ile Ile Glu Gln Met Ser Ser Ser Ser Gly Ser Ser Ser Ser Asp  
 85 90 95

Ser Glu Ser Ser Ser Gly Ser Asp Asp Asp Ser Ser Ser Ser Gly Gly  
 100 105 110

Glu Xaa Asn Gly Pro Ala Ser Xaa Pro Gln Xaa Xaa His Gln Gln Pro  
 115 120 125

Tyr Asn Ser Arg Pro Ala Val Ala Asn Gly Thr Ser Arg Pro Gln Gly  
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Ser Asn Gln Xaa Met Asn Thr Leu Arg Asn Asp Leu Gln Leu Ser Glu  
 145 150 155 160

Xaa Gly Ser Asp Ser Asp Asp  
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<210> 185  
 <211> 4582  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 185

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&lt;210&gt; 186

&lt;211&gt; 1461

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (364)

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (369)

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (1433)

&lt;400&gt; 186

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Met Ser Pro Ile Met Thr Ser Pro His Ser Pro Gly Ala Ser Gly Asn
  1             5             10             15

```

```

Met Glu Arg Ile Thr Ser Pro Val Leu Met Gly Glu Glu Asn Asn Val
          20             25             30

```

```

Val His Asn Gln Lys Val Glu Ile Leu Arg Lys Met Leu Gln Lys Glu
          35             40             45

```

```

Gln Glu Arg Leu Gln Leu Leu Gln Glu Asp Tyr Asn Arg Thr Pro Ala
          50             55             60

```

```

Gln Arg Leu Leu Lys Glu Ile Gln Glu Ala Lys Lys His Ile Pro Gln
          65             70             75             80

```

```

Leu Gln Glu Gln Leu Ser Lys Ala Thr Gly Ser Ala Gln Asp Gly Ala
          85             90             95

```

```

Val Val Thr Pro Ser Arg Pro Leu Gly Asp Thr Leu Thr Val Ser Glu
          100            105            110

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```

Ala Glu Thr Asp Pro Gly Asp Val Leu Gly Arg Thr Asp Cys Ser Ser

```

115	120	125
Gly Asp Ala Ser Arg Pro Ser Ser Asp Asn Ala Asp Ser Pro Lys Ser 130 135 140		
Gly Pro Lys Glu Arg Ile Tyr Leu Glu Glu Asn Pro Glu Lys Ser Glu 145 150 155 160		
Thr Ile Gln Asp Thr Asp Thr Gln Ser Leu Val Gly Ser Pro Ser Thr 165 170 175		
Arg Ile Ala Pro His Ile Ile Gly Ala Glu Asp Asp Asp Phe Gly Thr 180 185 190		
Glu His Glu Gln Ile Asn Gly Gln Cys Ser Cys Phe Gln Ser Ile Glu 195 200 205		
Leu Leu Lys Ser Arg Pro Ala His Leu Ala Val Phe Leu His His Val 210 215 220		
Val Ser Gln Phe Asp Pro Ala Thr Leu Leu Cys Tyr Leu Tyr Ser Asp 225 230 235 240		
Leu Tyr Lys His Thr Asn Ser Lys Glu Thr Arg Arg Ile Phe Leu Glu 245 250 255		
Phe His Gln Phe Phe Leu Asn Arg Ser Ala His Leu Lys Val Ser Val 260 265 270		
Pro Asp Glu Met Ser Ala Asp Leu Glu Lys Arg Arg Pro Glu Leu Ile 275 280 285		
Pro Glu Asp Leu His Arg His Tyr Ile Gln Thr Met Gln Glu Arg Val 290 295 300		
His Pro Glu Val Gln Arg His Leu Lys Asp Phe Arg Gln Lys Arg Ser 305 310 315 320		
Met Gly Leu Thr Leu Ala Glu Ser Glu Leu Thr Lys Leu Asp Ala Glu 325 330 335		
Arg Asp Lys Asp Arg Leu Thr Leu Glu Lys Glu Arg Thr Cys Ala Glu 340 345 350		
Gln Ile Val Ala Lys Ile Glu Glu Val Leu Met Xaa Ala Gln Ala Val 355 360 365		
Xaa Glu Asp Lys Ser Ser Thr Met Gln Tyr Val Ile Leu Met Tyr Met 370 375 380		
Lys His Leu Gly Val Lys Val Lys Glu Pro Arg Asn Leu Glu His Lys 385 390 395 400		
Arg Gly Arg Ile Gly Phe Leu Pro Lys Ile Lys Gln Ser Met Lys Lys 405 410 415		
Asp Lys Glu Gly Glu Glu Lys Gly Lys Arg Arg Gly Phe Pro Ser Ile 420 425 430		
Leu Gly Pro Pro Arg Arg Pro Ser Arg His Asp Asn Ser Ala Ile Gly		

435	440	445
Arg Ala Met Glu Leu Gln Lys	Ala Arg His Pro Lys His Leu Ser Thr	
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Pro Ser Ser Val Ser Pro Glu Pro Gln Asp Ser Ala Lys Leu Arg Gln		
465	470	475
Ser Gly Leu Ala Asn Glu Gly Thr Asp Ala Gly Tyr Leu Pro Ala Asn		
485	490	495
Ser Met Ser Ser Val Ala Ser Gly Ala Ser Phe Ser Gln Glu Gly Gly		
500	505	510
Lys Glu Asn Asp Thr Gly Ser Lys Gln Val Gly Glu Thr Ser Ala Pro		
515	520	525
Gly Asp Thr Leu Asp Gly Thr Pro Arg Thr Leu Asn Thr Val Phe Asp		
530	535	540
Phe Pro Pro Pro Pro Leu Asp Gln Val Gln Glu Glu Glu Cys Glu Val		
545	550	555
Glu Arg Val Thr Glu His Gly Thr Pro Lys Pro Phe Arg Lys Phe Asp		
565	570	575
Ser Val Ala Phe Gly Glu Ser Gln Ser Glu Asp Glu Gln Phe Glu Asn		
580	585	590
Asp Leu Glu Thr Asp Pro Pro Asn Trp Gln Gln Leu Val Ser Arg Glu		
595	600	605
Val Leu Leu Gly Leu Lys Pro Cys Glu Ile Lys Arg Gln Glu Val Ile		
610	615	620
Asn Glu Leu Phe Tyr Thr Glu Arg Ala His Val Arg Thr Leu Lys Val		
625	630	635
Leu Asp Gln Val Phe Tyr Gln Arg Val Ser Arg Glu Gly Ile Leu Ser		
645	650	655
Pro Ser Glu Leu Arg Lys Ile Phe Ser Asn Leu Glu Asp Ile Leu Gln		
660	665	670
Leu His Ile Gly Leu Asn Glu Gln Met Lys Ala Val Arg Lys Arg Asn		
675	680	685
Glu Thr Ser Val Ile Asp Gln Ile Gly Glu Asp Leu Leu Thr Trp Phe		
690	695	700
Ser Gly Pro Gly Glu Glu Lys Leu Lys His Ala Ala Ala Thr Phe Cys		
705	710	715
Ser Asn Gln Pro Phe Ala Leu Glu Met Ile Lys Ser Arg Gln Lys Lys		
725	730	735
Asp Ser Arg Phe Gln Thr Phe Val Cln Asp Ala Glu Ser Asn Pro Leu		
740	745	750
Cys Arg Arg Leu Gln Leu Lys Asp Ile Ile Pro Thr Gln Met Gln Arg		



755					760					765				
Leu Thr Lys Tyr Pro	Leu Leu Leu Asp Asn Ile	Ala Lys Tyr Thr Glu	770	775	780									
Trp Pro Thr Glu Arg	Glu Lys Val Lys Lys	Ala Ala Asp His Cys Arg	785	790	795	800								
Gln Ile Leu Asn Tyr	Val Asn Gln Ala Val	Lys Glu Ala Glu Asn Lys	805	810	815									
Gln Arg Leu Glu Asp	Tyr Gln Arg Arg Leu	Asp Thr Ser Ser Leu Lys	820	825	830									
Leu Ser Glu Tyr Pro	Asn Val Glu Glu Leu	Arg Asn Leu Asp Leu Thr	835	840	845									
Lys Arg Lys Met Ile	His Glu Gly Pro Leu	Val Trp Lys Val Asn Arg	850	855	860									
Asp Lys Thr Ile Asp	Leu Tyr Thr Leu Leu	Glu Asp Ile Leu Val	865	870	875	880								
Leu Leu Gln Lys Gln	Asp Asp Arg Leu Val	Leu Arg Cys His Ser Lys	885	890	895									
Ile Leu Ala Ser Thr	Ala Asp Ser Lys His	Thr Phe Ser Pro Val Ile	900	905	910									
Lys Leu Ser Thr Val	Leu Val Arg Gln Val	Ala Thr Asp Asn Lys Ala	915	920	925									
Leu Phe Val Ile Ser	Met Ser Asp Asn Gly	Ala Gln Ile Tyr Glu Leu	930	935	940									
Val Ala Gln Thr Val	Ser Glu Lys Thr Val	Trp Gln Asp Leu Ile Cys	945	950	955	960								
Arg Met Ala Ala Ser	Val Lys Glu Gln Ser	Thr Lys Pro Ile Pro Leu	965	970	975									
Pro Gln Ser Thr Pro	Gly Glu Gly Asp Asn	Asp Glu Glu Asp Pro Ser	980	985	990									
Lys Leu Lys Glu Glu	Gln His Gly Ile Ser	Val Thr Gly Leu Gln Ser	995	1000	1005									
Pro Asp Arg Asp Leu	Gly Leu Glu Ser Thr	Leu Ile Ser Ser Lys Pro	1010	1015	1020									
Gln Ser His Ser Leu	Ser Thr Ser Gly Lys	Ser Glu Val Arg Asp Leu	1025	1030	1035	1040								
Phe Val Ala Glu Arg	Gln Phe Ala Lys Glu	Gln His Thr Asp Gly Thr	1045	1050	1055									
Leu Lys Glu Val Gly	Glu Asp Tyr Gln Ile	Ala Ile Pro Asp Ser His	1060	1065	1070									
Leu Pro Val Ser Glu	Glu Arg Trp Ala Leu	Asp Ala Leu Arg Asn Leu												

1075	1080	1085
Gly Leu Leu Lys Gln Leu Leu Val Gln Gln Leu Gly Leu Thr Glu Lys 1090	1095	1100
Ser Val Gln Glu Asp Trp Gln His Phe Pro Arg Tyr Arg Thr Ala Ser 1105	1110	1115 1120
Gln Gly Pro Gln Thr Asp Ser Val Ile Gln Asn Ser Glu Asn Ile Lys 1125	1130	1135
Ala Tyr His Ser Gly Glu Gly His Met Pro Phe Arg Thr Gly Thr Gly 1140	1145	1150
Asp Ile Ala Thr Cys Tyr Ser Pro Arg Thr Ser Thr Glu Ser Phe Ala 1155	1160	1165
Pro Arg Asp Ser Val Gly Leu Ala Pro Gln Asp Ser Gln Ala Ser Asn 1170	1175	1180
Ile Leu Val Met Asp His Met Ile Met Thr Pro Glu Met Pro Thr Met 1185	1190	1195 1200
Glu Pro Glu Gly Gly Leu Asp Asp Ser Gly Glu His Phe Phe Asp Ala 1205	1210	1215
Arg Glu Ala His Ser Asp Glu Asn Pro Ser Glu Gly Asp Gly Ala Val 1220	1225	1230
Asn Lys Glu Glu Lys Asp Val Asn Leu Arg Ile Ser Gly Asn Tyr Leu 1235	1240	1245
Ile Leu Asp Gly Tyr Asp Pro Val Gln Glu Ser Ser Thr Asp Glu Glu 1250	1255	1260
Val Ala Ser Ser Leu Thr Leu Gln Pro Met Thr Gly Ile Pro Ala Val 1265	1270	1275 1280
Glu Ser Thr His Gln Gln Gln His Ser Pro Gln Asn Thr His Ser Asp 1285	1290	1295
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Gly Ala Met Glu Tyr Ser Cys Phe Glu Ile Gln Ser Pro Ser Ser Cys 1315	1320	1325
Ala Asp Ser Gln Ser Gln Ile Met Glu Tyr Ile His Lys Ile Glu Ala 1330	1335	1340
Asp Leu Glu His Leu Lys Glu Gly Gly Gly Lys Leu Thr Pro Phe Phe 1345	1350	1355 1360
Ala Lys Gly Trp Leu Asp Gln Pro Ser Gln Thr Ser Thr Gln Ile Lys 1365	1370	1375
Val Arg Ala Ala Cys Pro Gly Gly Asp Cys Arg Leu Leu Asp Leu Glu 1380	1385	1390
Tyr Arg Pro Cys Leu Thr Thr Ser Trp Leu Gln Cys Gly Cys Arg Glu		

1395                      1400                      1405  
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 1410                      1415                      1420  
 Gln Gly Ala Gln Ser Gly Thr Ser Xaa Ser Gln Cys Gly Ser Cys Thr  
 1425                      1430                      1435                      1440  
 Asn Leu Phe Val Arg Glu Tyr Pro Phe Pro His Ser Thr Leu Leu Thr  
 1445                      1450                      1455  
 Ile Gly Asn Ser Phe  
 1460

<210> 187  
 <211> 2837  
 <212> DNA  
 <213> Homo sapiens

<400> 187  
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 ggggtgacatt ccatgggacg acaaggattt caggatgttc tctctctgga ctgctctgtt 300  
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aaaaaaaaaa aaaaaaa 2837

```

&lt;210&gt; 188

&lt;211&gt; 686

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 188

```

Met Gly Glu Lys Lys Glu Ser Lys Pro Ala Ala Thr Thr Arg Ser Ser
  1             5             10             15

```

```

Gly Gly Gly Gly Gly Gly Gly Gly Lys Arg Gly Gly Lys Lys Asp Asp
      20             25             30

```

```

Ser His Trp Trp Ser Arg Phe Gln Lys Gly Asp Ile Pro Trp Asp Asp
      35             40             45

```

```

Lys Asp Phe Arg Met Phe Phe Leu Trp Thr Ala Leu Phe Trp Gly Gly
      50             55             60

```

```

Val Met Phe Tyr Leu Leu Leu Lys Arg Ser Gly Arg Glu Ile Thr Trp
      65             70             75             80

```

```

Lys Asp Phe Val Asn Asn Tyr Leu Ser Lys Gly Val Val Asp Arg Leu
      85             90             95

```

```

Glu Val Val Asn Lys Arg Phe Val Arg Val Thr Phe Thr Pro Gly Lys
      100            105            110

```

```

Thr Pro Val Asp Gly Gln Tyr Val Trp Phe Asn Ile Gly Ser Val Asp
      115            120            125

```

```

Thr Phe Glu Arg Asn Leu Glu Thr Leu Gln Gln Glu Leu Gly Ile Glu
      130            135            140

```

```

Gly Glu Asn Arg Val Pro Val Val Tyr Ile Ala Glu Ser Asp Gly Ser
      145            150            155            160

```

```

Phe Leu Leu Ser Met Leu Pro Thr Val Leu Ile Ile Ala Phe Leu Leu
      165            170            175

```

```

Tyr Thr Ile Arg Arg Gly Pro Ala Gly Ile Gly Arg Thr Gly Arg Gly
      180            185            190

```

```

Met Gly Gly Leu Phe Ser Val Gly Glu Thr Thr Ala Lys Val Leu Lys
      195            200            205

```

```

Asp Glu Ile Asp Val Lys Phe Lys Asp Val Ala Gly Cys Glu Glu Ala
      210            215            220

```

```

Lys Leu Glu Ile Met Glu Phe Val Asn Phe Leu Lys Asn Pro Lys Gln
      225            230            235            240

```

Tyr Gln Asp Leu Gly Ala Ile Ile Pro Lys Gly Ala Ile Leu Thr Gly  
 245 250 255  
 Pro Pro Gly Thr Gly Lys Thr Leu Leu Ala Lys Ala Thr Ala Gly Glu  
 260 265 270  
 Ala Asn Val Pro Phe Ile Thr Val Ser Gly Ser Glu Phe Leu Glu Met  
 275 280 285  
 Phe Val Gly Val Gly Pro Ala Arg Val Arg Asp Leu Phe Ala Leu Ala  
 290 295 300  
 Arg Lys Asn Ala Pro Cys Ile Leu Phe Ile Asp Glu Ile Asp Ala Val  
 305 310 315 320  
 Gly Arg Lys Arg Gly Arg Gly Asn Phe Gly Gly Gln Ser Glu Gln Glu  
 325 330 335  
 Asn Thr Leu Asn Gln Leu Leu Val Glu Met Asp Gly Phe Asn Thr Thr  
 340 345 350  
 Thr Asn Val Val Ile Leu Ala Gly Thr Asn Arg Pro Gly Pro Pro Asp  
 355 360 365  
 Ile Lys Gly Arg Ala Ser Ile Phe Lys Val His Leu Arg Pro Leu Lys  
 370 375 380  
 Leu Asp Ser Thr Leu Glu Lys Asp Lys Leu Ala Arg Lys Leu Ala Ser  
 385 390 395 400  
 Leu Thr Pro Gly Phe Ser Gly Ala Asp Val Ala Asn Val Cys Asn Glu  
 405 410 415  
 Ala Ala Leu Ile Ala Ala Arg His Leu Ser Asp Ser Ile Asn Gln Lys  
 420 425 430  
 His Phe Glu Gln Ala Ile Glu Arg Val Ile Gly Gly Leu Lys Lys Lys  
 435 440 445  
 Thr Gln Val Leu Gln Pro Glu Glu Lys Lys Thr Val Ala Tyr His Glu  
 450 455 460  
 Ala Gly His Ala Val Ala Gly Trp Tyr Leu Glu His Ala Asp Pro Leu  
 465 470 475 480  
 Leu Lys Val Ser Ile Ile Pro Arg Gly Lys Gly Leu Gly Tyr Ala Gln  
 485 490 495  
 Tyr Leu Pro Lys Glu Gln Tyr Leu Tyr Thr Lys Glu Gln Leu Leu Asp  
 500 505 510  
 Arg Met Cys Met Thr Leu Gly Gly Arg Val Ser Glu Glu Ile Phe Phe  
 515 520 525  
 Gly Arg Ile Thr Thr Gly Ala Gln Asp Asp Leu Arg Lys Val Thr Gln  
 530 535 540  
 Ser Ala Tyr Ala Gln Ile Val Gln Phe Gly Met Asn Glu Lys Val Gly  
 545 550 555 560

Gln Ile Ser Phe Asp Leu Pro Arg Gln Gly Asp Met Val Leu Glu Lys  
565 570 575

Pro Tyr Ser Glu Ala Thr Ala Arg Leu Ile Asp Asp Glu Val Arg Ile  
580 585 590

Leu Ile Asn Asp Ala Tyr Lys Arg Thr Val Ala Leu Leu Thr Glu Lys  
595 600 605

Lys Ala Asp Val Glu Lys Val Ala Leu Leu Leu Leu Glu Lys Glu Val  
610 615 620

Leu Asp Lys Asn Asp Met Val Glu Leu Leu Gly Pro Arg Pro Phe Ala  
625 630 635 640

Glu Lys Ser Thr Tyr Glu Glu Phe Val Glu Gly Thr Gly Ser Leu Asp  
645 650 655

Glu Asp Thr Ser Leu Pro Glu Gly Leu Lys Asp Trp Asn Lys Glu Arg  
660 665 670

Glu Lys Glu Lys Glu Glu Pro Pro Gly Glu Lys Val Ala Asn  
675 680 685

<210> 189  
<211> 627  
<212> DNA  
<213> Homo sapiens

<400> 189  
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tgtgcggtaa atagagagtg gatggaaatt aaccctagaa aggatagttg taacttttaa 120  
aaagttgatt aactatttcg tgtgctaatt tgagtttttc tgaatactcc aatattggtt 180  
cctttaacac ctgtcttcag tttaacaatca cctaacttcc cagcggttgg gtctttttct 240  
ctgtctgacc ctgtcttatt tctcctacaa agacatatcc tgcgctgtac ttcagatact 300  
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gaggatctgg tcattttatg aaaggggcaa ttaaggggaa atggaagcag atctttttaa 420  
gaaggagcat ttgaaattag cccaggaatc atgtccggcg agtcctgctc ttttgtacct 480  
gggcataata gtcagccaca cagagctaga gtttagttcaa gaattgtctt tcttgatcgt 540  
gctatatatt tggaaacacg ttagatacag aggttaagatg tcaaaattct gaaatacaca 600  
caatatagga tcaaaaaaaaa aaaaaaa 627

<210> 190  
<211> 63  
<212> PRT  
<213> Homo sapiens

<400> 190  
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1 5 10 15

Ser Cys Pro Ala Ser Pro Ala Leu Leu Tyr Leu Gly Ile Ile Val Ser  
20 25 30

His Thr Glu Leu Glu Leu Val Gln Glu Leu Ser Phe Leu Ile Val Leu  
35 40 45

Tyr Phe Trp Lys His Val Arg Tyr Arg Gly Lys Met Ser Lys Phe

50

55

60

<210> 191  
 <211> 868  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (733)

<400> 191  
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 ctggctccat tggcttctcc ctgcaccagc cctgtcctca ggggtcagga aaaagcacac 180  
 agctttcttt cctctcctcc agaggcctgg aagggtgagtg gaggtccagt aagggtcctg 240  
 ctgccttgga tttcttggc' ctgccttgcc aactgcacc tgtagctcct gtcctctgtg 300  
 accccagaac agaggtgctg ccttccctgt ctcctagaca aagcacaag ggatgccctg 360  
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 gtgtgtgaag gangtgtgtg agcaggccca atcctttgca gcaagaatga gaggtcagag 780  
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 cccaagcact ggcagctttg cagccctc 868

<210> 192  
 <211> 107  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (62)

<400> 192  
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 1 5 10 15  
 Leu Ser Thr Thr Cys Thr Arg Gly Arg Gly Val Asn Lys Ile Pro Phe  
 20 25 30  
 Cys Leu Gly Gly Arg Pro Leu Pro Met Gly Leu Ala Ile Ser Arg Lys  
 35 40 45  
 Ala Pro Gln Ser Ser Ser Leu Phe Trp Leu Cys Val Lys Xaa Val Cys  
 50 55 60  
 Glu Gln Ala Gln Ser Phe Ala Ala Arg Met Arg Gly Gln Ser Ile Pro  
 65 70 75 80  
 Leu His Thr His Pro Gly Ala Asp Arg Leu Val Pro Pro Ser Leu His  
 85 90 95  
 Ala Cys Pro Ser Thr Gly Ser Phe Ala Ala Pro  
 100 105

<210> 193  
 <211> 467  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (57)

<220>  
 <221> unsure  
 <222> (254)

<400> 193  
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 tttattcagg ctgnttcccc acagcaccgg caggaaatga aggtgcactt atatgcatcc 300  
 ctgcaggaaat aaagagtggg tggcctgccc agcccagcac cacagccttt ccccagccag 360  
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 gagccagccc ctcaggaatt gcctcaaaag agaaaaaaaa aaaaaaa 467

<210> 194  
 <211> 1035  
 <212> DNA  
 <213> Homo sapiens

<400> 194  
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<210> 195  
 <211> 179  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (37)

<220>  
 <221> UNSURE



&lt;222&gt; (73)

&lt;400&gt; 195

Met Cys Leu Trp Arg Met Arg Lys Gly Leu Glu Ala Pro Arg Leu Arg  
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Phe Asn Tyr Ala Thr Trp Lys His Lys Glu Met Leu Leu Ser Arg Cys  
 20 25 30

Pro Ser Ser Cys Xaa Ala Ser Ser Ile Pro Ala Ala Ala Ser Glu Arg  
 35 40 45

Lys Ser Leu Leu Ile Cys Gln Lys Phe His Ser Val Gly Ser Asn Gly  
 50 55 60

Leu Leu Asp Phe Asp Ser Glu Tyr Xaa Glu Leu Trp Asp Trp Leu Ile  
 65 70 75 80

Asp Met Glu Ser Leu Val Met Asp Ser His Asp Leu Met Met Ser Glu  
 85 90 95

Glu Gln Gln Gln His Leu Tyr Lys Arg Tyr Ser Val Glu Met Ser Ile  
 100 105 110

Arg His Leu Lys Lys Thr Glu Leu Leu Ser Lys Val Glu Ala Leu Lys  
 115 120 125

Lys Gly Gly Val Leu Leu Pro Asn Asp Leu Leu Glu Lys Val Asp Ser  
 130 135 140

Ile Asn Glu Lys Trp Glu Leu Leu Gly Val Phe Ala Phe Leu Leu Leu  
 145 150 155 160

Phe Val Gly Tyr Val Tyr Ile Phe Cys Val Val Lys Tyr Ser Val Arg  
 165 170 175

Phe Leu Ile

&lt;210&gt; 196

&lt;211&gt; 3831

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 196

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caaaaacaaag atgcaaatct gacccaaatc tgaattgcag aattgaaatca gcctgtgttt 3780
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&lt;210&gt; 197

&lt;211&gt; 1075

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 197

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1

5

10

15

Asp Pro Met Ala Thr Asp Ala Ser Pro Met Ala Ile Asn Met Thr Pro  
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 Thr Val Glu Gln Gly Glu Gly Glu Glu Ala Met Lys Asp Met Asp Ser  
 35 40 45  
 Asp Gln Gln Tyr Glu Lys Pro Pro Pro Leu His Thr Gly Ala Asp Trp  
 50 55 60  
 Lys Ile Val Leu His Leu Pro Glu Ile Glu Thr Trp Leu Arg Met Thr  
 65 70 75 80  
 Ser Glu Arg Val Arg Asp Leu Thr Tyr Ser Val Gln Gln Asp Ser Asp  
 85 90 95  
 Ser Lys His Val Asp Val His Leu Val Gln Leu Lys Asp Ile Cys Glu  
 100 105 110  
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 115 120 125  
 Phe Ser Leu Lys Leu Leu Ser Tyr Ser Val Asn Val Ile Val Asp Ile  
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 His Ala Val Gln Leu Leu Trp His Gln Leu Arg Val Ser Val Leu Val  
 145 150 155 160  
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 165 170 175  
 Thr Arg Gln Thr Asp Ile Leu Gln Ala Phe Ser Glu Glu Thr Lys Glu  
 180 185 190  
 Gly Arg Leu Asp Ser Leu Thr Glu Val Asp Asp Ser Gly Gln Leu Thr  
 195 200 205  
 Ile Lys Cys Ser Gln Asn Tyr Leu Ser Leu Asp Cys Gly Ile Thr Ala  
 210 215 220  
 Phe Glu Leu Ser Asp Tyr Ser Pro Ser Glu Asp Leu Leu Ser Gly Leu  
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 Gly Asp Met Thr Ser Ser Gln Val Lys Thr Lys Pro Phe Asp Ser Trp  
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 Ser Tyr Ser Glu Met Glu Lys Glu Phe Pro Glu Leu Ile Arg Ser Val  
 260 265 270  
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 325 330 335

Ala Gln Pro Ser Ser Glu Thr Val Gln Gln Glu Ser Ser Ser Ser Ser  
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 His His Asp Ala Lys Asn Gln Gln Pro Val Pro Cys Glu Asn Ala Thr  
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 Pro Lys Arg Thr Ile Arg Asp Cys Phe Asn Tyr Asn Glu Asp Ser Pro  
 370 375 380  
 Thr Gln Pro Thr Leu Pro Lys Arg Gly Leu Phe Leu Lys Glu Glu Thr  
 385 390 395 400  
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 Pro Ser Ala Ala Ser Gln Ser Tyr Glu Cys Leu His Lys Val Gly Asn  
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 465 470 475 480  
 Ser Leu Gly Arg Leu Asn Asp Cys Tyr Lys Glu Lys Ser Arg Leu Lys  
 485 490 495  
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 545 550 555 560  
 Ser Trp Asn Ala Lys Leu Gln Leu Gln Ser Glu Thr Ser Ser Ser Pro  
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 Ala Phe Thr Gln Ser Ser Glu Ser Ser Val Gly Ser Asp Asn Ile Met  
 580 585 590  
 Ser Pro Val Pro Leu Leu Ser Lys His Lys Ser Lys Lys Gly Gln Ala  
 595 600 605  
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 610 615 620  
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Lys Pro Arg Gly Glu Thr Ile Gln Asn Ile Asp Asp Trp Glu Leu Ser  
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 Lys His Thr Arg Leu Gly Arg Val Ser Pro Ser Ser Ser Ser Asp Ile  
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 740 745 750  
 His Ser Ala Thr Lys Ser Ala Leu Ile Gln Lys Leu Met Gln Asp Ile  
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 770 775 780  
 Val Asn Lys Leu Asp Glu Phe Ile Gln Trp Leu Asn Glu Ala Met Glu  
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 Cys Ala Leu Lys Glu Ala Val Glu Glu Gly His Gln Leu Leu Glu  
 835 840 845  
 Leu Ile Ala Ser His Lys Ala Gly Leu Lys Asp Met Leu Arg Met Ile  
 850 855 860  
 Ala Ser Gln Trp Lys Glu Leu Gln Arg Gln Ile Lys Arg Gln His Ser  
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 Trp Ile Leu Arg Ala Leu Asp Thr Ile Lys Ala Glu Ile Leu Ala Thr  
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 Ser Leu Lys Leu Tyr Ser Glu Gln Tyr Thr Ser Ser Ser Lys Arg Lys  
 930 935 940  
 Glu Glu Phe Ala Asp Met Ser Lys Val His Ser Val Gly Ser Asn Gly  
 945 950 955 960  
 Leu Leu Asp Phe Asp Ser Glu Tyr Gln Glu Leu Trp Asp Trp Leu Ile  
 965 970 975

Asp Met Glu Ser Leu Val Met Asp Ser His Asp Leu Met Met Ser Glu  
 980 985 990

Glu Gln Gln Gln His Leu Tyr Lys Arg Tyr Ser Val Glu Met Ser Ile  
 995 1000 1005

Arg His Leu Lys Lys Thr Glu Leu Leu Ser Lys Val Glu Ala Leu Lys  
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Lys Gly Gly Val Leu Leu Pro Asn Asp Leu Leu Glu Lys Val Asp Ser  
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Ile Asn Glu Lys Trp Glu Leu Leu Gly Val Phe Ala Phe Leu Leu Leu  
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Phe Leu Ile  
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 cttttgatcg caatacagaa tctctctttg aagaactgtc ttcagctggc tcaggcctaa 240  
 taggagatgt ggatgaagga gcagatttac taggaatggg tcgggaagtt gagaatctta 300  
 tattagaaaa tacacaactg ttggaaacca aaaaatgcttt gaacatagtg aagaatgatt 360  
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 ggaaagctcg ggcagaagct gaagatgcag ggcaaaaagc aaaagatgac gatgatagtg 540  
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&lt;210&gt; 199

&lt;211&gt; 828

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 199

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Ala Asp Leu Leu Gly Met Gly Arg Glu Val Glu Asn Leu Ile Leu Glu
          50              55              60

Asn Thr Gln Leu Leu Glu Thr Lys Asn Ala Leu Asn Ile Val Lys Asn
          65              70              75              80

Asp Leu Ile Ala Lys Val Asp Glu Leu Thr Cys Glu Lys Asp Val Leu
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Gln Gly Glu Leu Glu Ala Val Lys Gln Ala Lys Leu Lys Leu Glu Glu
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Lys Asn Arg Glu Leu Glu Glu Leu Arg Lys Ala Arg Ala Glu Ala
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Glu Asp Ala Gly Gln Lys Ala Lys Asp Asp Asp Asp Ser Asp Ile Pro
          130              135              140

Thr Ala Gln Arg Lys Arg Phe Thr Arg Val Glu Met Ala Arg Val Leu
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Met Glu Arg Asn Gln Tyr Lys Glu Arg Leu Met Glu Leu Gln Glu Ala
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 Phe Leu Ser Glu Glu Thr Glu Ala Ser Leu Ala Ser Arg Arg Glu Gln  
 260 265 270  
 Lys Arg Glu Gln Tyr Arg Gln Val Lys Ala His Val Gln Lys Glu Asp  
 275 280 285  
 Gly Arg Val Gln Ala Phe Gly Trp Ser Leu Pro Gln Lys Tyr Lys Gln  
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 Val Tyr Leu Arg Pro Leu Asp Glu Lys Asp Thr Ser Met Lys Leu Trp  
 325 330 335  
 Cys Ala Val Gly Val Asn Leu Ser Gly Gly Lys Thr Arg Asp Gly Gly  
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 Ser Val Val Gly Ala Ser Val Phe Tyr Lys Asp Val Ala Gly Leu Asp  
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 370 375 380  
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 385 390 395 400  
 Glu Leu Ser Ser Leu Val Trp Ile Cys Thr Ser Thr His Ser Ala Thr  
 405 410 415  
 Lys Val Leu Ile Ile Asp Ala Val Gln Pro Gly Asn Ile Leu Asp Ser  
 420 425 430  
 Phe Thr Val Cys Asn Ser His Val Leu Cys Ile Ala Ser Val Pro Gly  
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 Ala Arg Glu Thr Asp Tyr Pro Ala Gly Glu Asp Leu Ser Glu Ser Gly  
 450 455 460  
 Gln Val Asp Lys Ala Ser Leu Cys Gly Ser Met Thr Ser Asn Ser Ser  
 465 470 475 480  
 Ala Glu Thr Asp Ser Leu Leu Gly Gly Ile Thr Val Val Gly Cys Ser  
 485 490 495



Ala Glu Gly Val Thr Gly Ala Ala Thr Ser Pro Ser Thr Asn Gly Ala  
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 Ser Pro Val Met Asp Lys Pro Pro Glu Met Glu Ala Glu Asn Ser Glu  
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 Val Tyr Thr Glu His Val Phe Thr Asp Pro Leu Gly Val Gln Ile Pro  
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 Glu Asp Leu Ser Pro Val Tyr Gln Ser Ser Asn Asp Ser Asp Ala Tyr  
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 Glu Ala Gln Lys Met Ser Ser Leu Leu Pro Thr Met Trp Leu Gly Ala  
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Lys Ala Gly Ala Thr Pro Ser Ser Leu Phe Ser Thr Gln His Gln Ala

35

40

45

Leu Ser Arg His Pro Ile Asn His Cys  
50 55



Applicant's or agent's file reference 1290.1001010	International application No. <b>PCT/US 00/25135</b>
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**INDICATIONS RELATING TO DEPOSITED MICROORGANISM  
OR OTHER BIOLOGICAL MATERIAL**

(PCT Rule 13bis)

A. The indications made below relate to the deposited microorganism or other biological material referred to in the description on pages <u>333</u> , line <u>35</u> to <u>35</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <b>AMERICAN TYPE CULTURE COLLECTION</b>	
Address of depositary institution (including postal code and country) <b>American Type Culture Collection (ATCC) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America</b>	
Date of deposit <b>see Attachment A</b>	Accession Number <b>see Attachment A</b>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input checked="" type="checkbox"/>	
In respect of those designations for which a European patent is sought, the Applicant(s) hereby informs the International Bureau that the Applicant wishes that, until the publication of the mention of the grant of a European patent or for 20 years from the date of filing if the application is refused or withdrawn or deemed to be withdrawn, the biological material deposited with the American Type Culture Collection under Accession No. <u>see Attachment A</u>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

<p>For receiving Office use only</p> <p><input checked="" type="checkbox"/> This sheet was received with the international application</p> <p>Authorized officer <i>B. H. H. H.</i></p>	<p>For International Bureau use only</p> <p><input type="checkbox"/> This sheet was received by the International Bureau on:</p> <p>Authorized officer</p>
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**INDICATIONS RELATING TO A DEPOSITED MICROORGANISM**  
**(Additional Sheet)**

**C. ADDITIONAL INDICATIONS (Continued)**

shall be made available as provided in ~~Rule 28(3) EPC only~~ by the issue of a sample to an expert nominated by the requester (Rule 28(4) EPC).

In respect of the designation of Australia in the subject PCT application, and in accordance with Regulation 3.25(3) of the Australian Patents Regulations, the Applicant hereby gives notice that the furnishing of a sample of the biological material deposited with the American Type Culture Collection under Accession No. ~~Attachment A~~<sup>EPC</sup> shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention and who is nominated in a request for the furnishing of a sample.

In respect of the designation of Canada in the subject PCT application, the Applicant hereby informs the International Bureau that the Applicant wishes that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the biological material deposited with the American Type Culture Collection under Accession No. ~~Attachment A~~<sup>EPC</sup> and referred to in the application to an independent expert nominated by the Commissioner.

## Attachment A

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Deposit of Clones

Clones AX65\_22, BD335\_14, BG241\_1, BL187\_4, BL249\_18, BO71\_1, BO365\_2, BV51\_1, BV140\_3, BV141\_2, CC194\_4, and DA136\_11 were deposited on October 3, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98196, from which each clone comprising a particular polynucleotide is obtainable.

Clones AR415\_4, AS63\_29, BG160\_1, BO432\_4, BO538\_2, BR595\_4, CI490\_2, CI522\_1, CN238\_1, CO390\_1, and AY304\_1 (an additional isolate of clone AY304\_14) were deposited on October 25, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98232, from which each clone comprising a particular polynucleotide is obtainable. Clone AY304\_14 was deposited on October 23, 1997 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and was given the accession number 98561.

Clones AJ20\_2, AR440\_1, AS164\_1, AX8\_1, BD176\_3, BD339\_1, BD427\_1, BL229\_22, BV123\_16, and CH377\_1 were deposited on November 15, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98261, from which each clone comprising a particular polynucleotide is obtainable.

Clones BD441\_1, BD441\_2, BG102\_3, BK158\_1, BP163\_1, BZ16\_3, CC182\_1, CG109\_1 and CJ397\_1 were deposited on November 20, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98264, from which each clone comprising a particular polynucleotide is obtainable.

Clones AM795\_4, AT340\_1, BG132\_1, BG219\_2, BG366\_2, BV172\_2, CC247\_10, CI480\_9, CO722\_1, and CT748\_2 were deposited on December 5, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98271, from which each clone comprising a particular polynucleotide is obtainable.

Clones AJ1\_1, AQ73\_3, BG142\_1, BV66\_1, BV291\_3, CK201\_1, CQ331\_2, CT550\_1, CT585\_1 and CT797\_3 were deposited on December 13, 1996 with the ATCC

## Attachment A

-2-

(American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98278, from which each clone comprising a particular polynucleotide is obtainable.

Clones CB107\_1, CG300\_3, CJ145\_1, CJ160\_11, CO20\_1, CO223\_1, CO310\_2, CP258\_3, CW1155\_3 and CZ247\_2 were deposited on December 17, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98279, from which each clone comprising a particular polynucleotide is obtainable. Clone CO223\_3 was deposited on January 9, 1997 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and was given the accession number 98291.

Clones AM666\_1, BN387\_3, BQ135\_2, CR678\_1, CW420\_2, CW795\_2, CW823\_3, DF989\_3, DL162\_2, DL162\_1, and EC172\_1 were deposited on January 10, 1997 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98292, from which each clone comprising a particular polynucleotide is obtainable.

## INTERNATIONAL SEARCH REPORT

International Application No

I US 00/25135

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C07K14/47 C12N1/21 C12N5/10 C12Q1/68  
A61K38/17

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, BIOSIS, STRAND

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X, L	<p>WO 98 17687 A (GENETICS INST) 30 April 1998 (1998-04-30) the document throws doubt on the priority of the application abstract; claims 20-22 see SEQ ID NO: 8 and 9 (pp.73-77) page 18, line 30 -page 20, line 2 page 23, line 12 -page 24, line 14 page 31, line 12 -page 64, line 16 -----</p>	1-11

☐ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

## \* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

14 December 2000

Date of mailing of the international search report

30.01.01

Name and mailing address of the ISA

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Authorized officer

Oderwald, H

# INTERNATIONAL SEARCH REPORT

national application No.  
PCT/US 00/25135

## Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-11

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

**FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210**

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

**1. Claims: 1-11**

An isolated polynucleotide comprising SEQ ID NO: 41 which encodes a protein of SEQ ID NO: 42 (BG160\_1). A host cell, a process for producing said protein, a protein produced by said process, a composition comprising said protein.

**2. Claims: 12, 13**

An isolated polynucleotide comprising SEQ ID NO: 129. A protein encoded by said polynucleotide having amino acid sequence SEQ ID NO: 130 (C0722\_1).

### Information on patent family members

F . US 00/25135

Form PCT/ISA/210 (patent family annex) (July 1992)